STIC-Biotech/ChemLib 1524743

From: Bunner, Bridget
Sent: Friday, May 27, 2005 10:09 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/777,524:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 1, 2005, 22:01:20 ; Search time 40 Seconds
(without alignments)
728.842 Million cell updates/sec

Title: US-10-777-524-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLPLLLPPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	144.5	9.1	823	2	S48394	probable membrane
2	123.5	7.8	1114	2	T49517	p63 related protei
3	118.5	7.4	509	2	JC5288	SHP substrate-1 pr
4	116	7.3	392	2	B44194	poliovirus recepto
5	116	7.3	417	2	A44194	poliovirus recepto
6	115.5	7.3	513	2	JC5289	SHP substrate-1 pr
7	114	7.2	392	1	RWHUPD	poliovirus recepto
8	114	7.2	417	1	RWHUPA	poliovirus recepto
9	112.5	7.1	403	2	I52590	m33-B isoform - mo
10	110	6.9	235	2	S25758	Ig lambda chain -
11	110	6.9	847	2	JH0371	B-cell adhesion pr
12	109.5	6.9	233	2	S25747	Ig lambda chain -
13	108.5	6.8	230	2	S49449	Ig lambda chain -
14	108.5	6.8	235	2	S14675	Ig lambda chain -
15	108.5	6.8	862	2	I49583	differentiation an
16	108.5	6.8	868	2	A46512	CD22 homolog/B lym
17	108	6.8	236	2	S25746	Ig lambda chain -
18	108	6.8	1694	2	S50065	sialoadhesin - mou
19	106	6.7	647	2	A35648	B-cell adhesion pr
20	106	6.7	710	2	A99486	ABC transporter, b
21	105.5	6.6	235	2	S25750	Ig lambda chain -
22	104.5	6.6	214	2	PC4156	Ig lambda chain V
23	104	6.5	231	2	S25751	Ig lambda chain -
24	104	6.5	798	2	T34248	hypothetical prote
25	103	6.5	446	2	T45525	WSC4 homolog [impo
26	103	6.5	469	2	S37483	Ig gamma-2a chain
27	102.5	6.4	407	2	T08732	hypothetical prote
28	102	6.4	572	2	B46529	Ig Y heavy chain (
29	101	6.3	118	2	E27889	Ig heavy chain V r
30	101	6.3	790	2	T34293	hypothetical prote
31	100.5	6.3	151	2	I46626	rearranged T-cell
32	100.5	6.3	152	2	B26471	Ig heavy chain pre
33	100	6.3	365	2	A47636	MHC class I histoc
34	100	6.3	365	2	I83063	A11.2 - human
35	100	6.3	365	2	I37478	MHC class I histoc
36	99.5	6.3	413	2	T04520	hypothetical prote
37	99	6.2	210	2	S25657	T-cell surface gly
38	99	6.2	231	2	S25738	Ig lambda chain -
39	99	6.2	232	2	S25756	Ig lambda chain -
40	98	6.2	217	2	JE0246	Ig lambda chain NI
41	98	6.2	235	2	S25759	Ig lambda chain -
42	97	6.1	142	2	A28344	VpreB protein prec
43	97	6.1	229	2	A20969	Ig kappa chain pre
44	97	6.1	365	2	I36961	MHC class I protei
45	97	6.1	1272	2	S26180	neurofascin - chic

ALIGNMENTS

RESULT 1
S48394
probable membrane protein YIL140w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48394; S50276
R;Churcher, C.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48310
A;Accession: S48394
A;Molecule type: DNA
A;Residues: 1-823 <CHU>
A;Cross-references: UNIPROT:P38928; GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763206; MI
R;Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W.
Yeast 10, 1503-1509, 1994
A;Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-
A;Reference number: S50275; MUID:95176709; PMID:7871890
A;Accession: S50276
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 80-823 <TOR>
A;Cross-references: EMBL:U07228; NID:g460247; PIDN:AAA67919.1; PID:g460249
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Genetics:
A;Gene: SGD:SRO4
A;Cross-references: SGD:S0001402; MIPS:YIL140w
A;Map position: 9L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YIL140w
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TM1>
F;511-527/Domain: transmembrane #status predicted <TM2>

Query Match 9.1%; Score 144.5; DB 2; Length 823;
Best Local Similarity 24.7%; Pred. No. 0.0026;
Matches 72; Conservative 45; Mismatches 96; Indels 79; Gaps 16;

```
Qy         25 TGSGPSYLYGV-TQPKHLSASM---GGSVEIPFSFYYPWELATAPDV-------RISWRR 73
              :|| |  | |  : | : | ||:    | |       |: :|: :  |:         |:  |
Db        308 SGSVPDELLGKNSNPANFSVSIYDTYGDV-----IYFNFEVVSTTDLFAISSLPNINATR 362

Qy         74 GHFHGQSFYSTRPPSIHKDYVNR----LFLN------WTEGQKS----------GFLRIS 113
              | :    |     ||   ||||      | |      | : | |           | ::|
Db        363 GEWFSYYFL----PSQFTDYVNTNVSLEFTNSSQDHDWVKFQSSNLTLAGEVPKNFDKLS 418

Qy        114 -----NLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWR 168
                  |   | | :||  : :|:: :      :   |: |     :|:|   :| | | :
Db        419 LGLKANQGSQSQELYFNIIGMDSKITHSNHSANATSTRSS---HHSTSTSSYTSSTYTAK 475

Qy        169 LSSTT---TTTGLRVTQGKRRSDSWHISLETAVGVAVAVTV-LGIMILGLIC-LLRWRRR 223
              :|||:   |::          :: | :   : || :|  | : ||:::: ||| |: ||||
Db        476 ISSTSAAATSSAPAALPAANKTSSHN---KKAVAIACGVAIPLGVILVALICFLIFWRRR 532
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Qy        224 KGQQRTK----------ATTPAREPFQNTEEPYENIRNEGQNTDPKLNPKDD 265
              :    :             || :| |             :|  |  || ||
Db        533 RENPDDENLPHAISGPDLNNPANKPNQ------------ENATPLNNPFDD 571


RESULT 2
T49517
p63 related protein [imported] - Neurospora crassa
N;Alternate names: protein B14D6.690
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49517
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1114 <SCH>
A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.690
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
A;Gene: NCSP:B14D6.690
A;Map position: 6
A;Introns: 132/2; 362/2; 427/3; 540/3

  Query Match             7.8%;  Score 123.5;  DB 2;  Length 1114;
  Best Local Similarity   23.1%;  Pred. No. 0.15;
  Matches   66;  Conservative   32;  Mismatches   81;  Indels  107;  Gaps   12;

Qy         26 GSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTR 85
              || |: |          |:|  | :  | ||       || ::|:|:          | |
Db        155 GSDPADL----------ATMTISDDKDFMFY-------APLIQINWQS---------SDR 188

Qy         86 PPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGT 145
              |              ||   || : :|             |::|| |:          |
Db        189 P--------------TETVFSGTVSLS-------------VDVDTMST--------LAT 212

Qy        146 KLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGKRRSDSWH-ISLETA--VGVAV 202
                  ||:    ||        :   ||   ::| :  |    :|| |   ||:||
Db        213 AGDAPAGVTSRVGFPSQSVVLVGSQGSNKPTG--ASEGNKEEDGVKPVSLSTGFKVGMAV 270

Qy        203 AVTVLGIMILGLICLLRWRRRKGQQR---------TKATTPAREPFQNTE---------- 243
              |  || : |: :| :  |||| |            |   |:  |:| |
Db        271 AGGVLAVAIVAIIFICAWRRRKQQMEEEEFDRMYGMKDVGPSTADFRNEEIPGWHRGPTR 330

Qy        244 ----EPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPS 285
                  | :  |::|::                | :  :|  |||
Db        331 RQPPAPVDPFRSDGES----------------ELMAPPAPYHPPS 359


RESULT 3
JC5288
SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JC5288
R;Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizatio
A;Reference number: JC5287; MUID:97223399; PMID:9070220
A;Contents: Brain
A;Accession: JC5288
A;Molecule type: mRNA
A;Residues: 1-509 <YAM>
A;Cross-references: DDBJ:D87967; NID:g1864012; PIDN:BAA13520.1; PID:g1864013
C;Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
 acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C;Genetics:
A;Gene: shps-1
A;Map position: 2

  Query Match             7.4%;  Score 118.5;  DB 2;  Length 509;
  Best Local Similarity   22.9%;  Pred. No. 0.15;
  Matches   57;  Conservative   44;  Mismatches   83;  Indels   65;  Gaps   13;

Qy         56 YYPWELATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNL 115
              :||        |::: |      :|     :  | :: |:       : |    | ||  |:
Db        279 FYP------EDLQLIWLE---NGNVSRNDTPKNLTKN------TDGTYNYTSLFLVNSSA 323

Qy        116 QKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTT 175
                ::|  |: |:|: |      ||                 |:|          |   |: ::
Db        324 HRED-VVFTCQVKHD------QQ------------PAITRN-------HTVLGLAHSSDQ 357

Qy        176 TGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPA 235
                ::   |   : :|::     :|| ||  :| ::::  : ||| :::| :  | :|
Db        358 GSMQTFPGNNATHNWNV----FIGVGVACALLVVLLMAALYLLRIKQKKAKGSTSST--- 410

Qy        236 REPFQNTEEPYENIRNEGQNTDPKLNPKDDGIVYASLAL--SSSTSPRAPPSHRPLKSPQ 293
                      || :| |   |  |   |  :| | || | |      :||||        |
Db        411 -----RLHEPEKNAREITQIQD--TNDIND-ITYADLNLPKEKKPAPRAP-------EPN 455

Qy        294 NETLYSVLK 302
              | | |: ::
Db        456 NHTEYASIE 464


RESULT 4
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no putat
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

  Query Match             7.3%;  Score 116;  DB 2;  Length 392;
  Best Local Similarity   21.2%;  Pred. No. 0.17;
  Matches   77;  Conservative   42;  Mismatches  110;  Indels  134;  Gaps   16;

Qy          4 PLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELAT 63
              |||| || |  ||          |:|      |  |  :   :| || :|      |    |
Db         11 PLLLTLLELSWPP--------PGTGDII---VQAPTQVPGFLGDSVTLPCYLQVPGMEET 59

Qy         64 APDVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQKSGF--------- 109
                 :::| |   ||:|     |: |: |           |::| ::  |
Db         60 HVS-QLTWSR---HGESGSMAVFHQTQGP-----------NYSEPKRLEFVAARLGTEL 103

Qy        110 ----LRISNLQKQDQSVYFC---------------RVELDTRSSGRQQWQSIEGTKLSI 149
                  ||:  |: :|:  | |                ||    :::   |   : |  : :
Db        104 RDASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLTGKPVPV 163

Qy        150 TQAVTTTTQRPSSMTTTWR--------------LSSTTTTTGLRVTQGKRRSDS----- 189
                : |:|  : |: :  ||                || | | | | :     : |
Db        164 ARCVSTGGRPPAHI--TWHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTC 221

Qy        190 --WHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYE 247
                  | | |    : | :||                                | : :   |:
Db        222 KVEHESFEKPQLLTVNLTVY----------------------------YPPEVSISGYD 252

Qy        248 N----IRNEGQNT-DPKLNPKDDGIVYASLALSSSTSPRAPPSH---------RPLKSPQ 293
              |      :||   | | : ||:  |  :      |:|    ||            ||:  |
Db        253 NNWYLSQNEATLTCDARSNPEPTGYNW------STTMGPLPPFAVAQGAQLLIRPVDKPI 306

Qy        294 NET 296
              | |
Db        307 NTT 309
```

```
RESULT 5
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: A44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>

  Query Match             7.3%;  Score 116;  DB 2;  Length 417;
  Best Local Similarity   21.2%;  Pred. No. 0.18;
  Matches   77;  Conservative   42;  Mismatches  110;  Indels  134;  Gaps   16;

Qy           4 PLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELAT 63
               |||| || |  ||          |:|     |  |  :  :| || :|     |    |
Db          11 PLLLTLLELSWPP--------PGTGDII---VQAPTQVPGFLGDSVTLPCYLQVPGMEET 59

Qy          64 APDVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQKSGF--------- 109
                 :::| |   ||:|     |: |: |            |::| ::  |
Db          60 HVS-QLTWSR---HGESGSMAVFHQTQGP-----------NYSEPKRLEFVAARLGTEL 103

Qy         110 ----LRISNLQKQDQSVYFC---------------RVELDTRSSGRQQWQSIEGTKLSI 149
                 ||:  |: :|:  | |                ||    :::   |  : |  : :
Db         104 RDASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLTGKPVPV 163

Qy         150 TQAVTTTTQRPSSMTTTWR--------------LSSTTTTTGLRVTQGKRRSDS----- 189
                 : |:|  : |: :  ||              || | | | | :     : |
Db         164 ARCVSTGGRPPAHI--TWHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTC 221

Qy         190 --WHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYE 247
                 | | |    : | :||                                | : :   |:
Db         222 KVEHESFEKPQLLTVNLTVY----------------------------YPPEVSISGYD 252

Qy         248 N----IRNEGQNT-DPKLNPKDDGIVYASLALSSSTSPRAPPSH---------RPLKSPQ 293
               |     :||   | | : ||:  | :      |:|    ||           ||:  |
Db         253 NNWYLSQNEATLTCDARSNPEPTGYNW------STTMGPLPPFAVAQGAQLLIRPVDKPI 306

Qy         294 NET 296
               | |
Db         307 NTT 309


RESULT 6
JC5289
SHP substrate-1 protein, 513 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC5289
R;Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizatior
A;Reference number: JC5287; MUID:97223399; PMID:9070220
A;Contents: Bzrain
A;Accession: JC5289
A;Molecule type: mRNA
A;Residues: 1-513 <YAM>
A;Cross-references: UNIPROT:P97797; DDBJ:D87968; NID:g1864014; PIDN:BAA13521.1; PID:g186
C;Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
 acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C;Genetics:
A;Gene: shps-1
A;Map position: 2

  Query Match             7.3%;  Score 115.5;  DB 2;  Length 513;
  Best Local Similarity   22.3%;  Pred. No. 0.25;
  Matches   56;  Conservative   46;  Mismatches   84;  Indels   65;  Gaps   13;

Qy          56 YYPWELATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNL 115
               :||       |::: |     :|    :  | :: |:       : |    | ||  |:
Db         279 FYP------EDLQLIWLE---NGNVSRNDTPKNLTKN------TDGTYNYTSLFLVNSSA 323

Qy         116 QKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTT 175
                ::|  |: |:|: |      ||           |:|       |   |: ::
Db         324 HRED-VVFTCQVKHD------QQ-----------PAITRN-------HTVLGLAHSSDQ 357

Qy         176 TGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPA 235
                 ::   |   : :|::     :|| ||  :| ::::  : ||| :::| :  | :|
Db         358 GSMQTFPGNNATHNWNV----FIGVGVACALLVVLLMAALYLLRIKQKKAKGSTSST--- 410

Qy         236 REPFQNTEEPYENIR--NEGQNTDPKLNPKDDGIVYASLAL--SSSTSPRAPPSHRPLKS 291
                       || :| |   : |:     |  :| | || | |      :||||
Db         411 -----RLHEPEKNAREITQVQSLIQDTNDIND-ITYADLNLPKEKKPAPRAP-------E 457

Qy         292 PQNETLYSVLK 302
               | | | |: ::
Db         458 PNNHTEYASIE 468


RESULT 7
RWHUPD
poliovirus receptor splice form delta precursor - human
N;Alternate names: poliovirus receptor H20B
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A43024; B31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: A43024
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P15151; EMBL:X64116
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: B31496
A;Molecule type: mRNA
A;Residues: 1-66,'A',68-392 <MEN>
A;Cross-references: GB:M24406
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-392/Product: poliovirus receptor delta #status predicted <MAT>
F;21-343/Domain: extracellular #status predicted <EXT>
F;42-125/Domain: immunoglobulin homology <IMM1>
F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-392/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

  Query Match             7.2%;  Score 114;  DB 1;  Length 392;
  Best Local Similarity   20.4%;  Pred. No. 0.24;
  Matches   71;  Conservative   46;  Mismatches  127;  Indels  104;  Gaps   14;
```

```
Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||: || |  ||         |:|      |  |   :   :| || :|     |  :
Db         12 LLVALLVLSWPP--------PGTGDVV---VQAPTQVPGFLGDSVTLPCYLQVP-NMEVT 59

Qy         65 PDVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQ-----KSGFLRISN 114
                :::| |   ||:|     |: |: ||    |     | :   :     ::  ||:
Db         60 HVSQLTWTR---HGESGSMAVFHQTQGPS----YSESKRLEFVAARLGAELRNASLRMFG 112

Qy        115 LQKQDQSVYFC----------------RVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQ 158
              |: :|:   | |              ||    :::   |   : |  : : : |:|  :
Db        113 LRVEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLTGEPVPMARCVSTGGR 172

Qy        159 RPSSMTTTWR---------------LSSTTTTTGLRVTQGKRRSDSWHISLETAVGVAVA 203
               |: :  ||                || | | | | :     : |  :::
Db        173 PPAQI--TWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVT---------- 220

Qy        204 VTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYENIRNEGQN-----TDP 258
                      | :    : |          | : :   |:|    |||      |
Db        221 ------------CKVEHESFEKPQLLTVNLTVYYPPEVSISGYDNNWYLGQNEATLTCDA 268

Qy        259 KLNPKDDGIVYASLALSSSTSPRAPPSH---------RPLKSPQNETL 297
              : ||:  |  :      |:|    ||           ||:  | | ||
Db        269 RSNPEPTGYNW------STTMGPLPPFAVAQGAQLLIRPVDKPINTTL 310
```

RESULT 8
RWHUPA
poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S12048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: S12048
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA454
A;Note: 67-Ala was also found
A;Note: the gamma form has 331-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
A;Molecule type: mRNA
A;Residues: 1-66,'A',68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Domain: immunoglobulin homology <IMM1>
F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 7.2%; Score 114; DB 1; Length 417;
Best Local Similarity 20.4%; Pred. No. 0.26;
Matches 71; Conservative 46; Mismatches 127; Indels 104; Gaps 14;

```
Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||: || |  ||         |:|      |  |   :   :| || :|     |  :
Db         12 LLVALLVLSWPP--------PGTGDVV---VQAPTQVPGFLGDSVTLPCYLQVP-NMEVT 59

Qy         65 PDVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQ-----KSGFLRISN 114
                :::| |   ||:|     |: |: ||    |     | :   :     ::  ||:
Db         60 HVSQLTWTR---HGESGSMAVFHQTQGPS----YSESKRLEFVAARLGAELRNASLRMFG 112

Qy        115 LQKQDQSVYFC----------------RVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQ 158
              |: :|:   | |              ||    :::   |   : |  : : : |:|  :
Db        113 LRVEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLTGEPVPMARCVSTGGR 172

Qy        159 RPSSMTTTWR---------------LSSTTTTTGLRVTQGKRRSDSWHISLETAVGVAVA 203
               |: :  ||                || | | | | :     : |  :::
Db        173 PPAQI--TWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVT---------- 220

Qy        204 VTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYENIRNEGQN-----TDP 258
                      | :    : |          | : :   |:|    |||      |
Db        221 ------------CKVEHESFEKPQLLTVNLTVYYPPEVSISGYDNNWYLGQNEATLTCDA 268

Qy        259 KLNPKDDGIVYASLALSSSTSPRAPPSH---------RPLKSPQNETL 297
              : ||:  |  :      |:|    ||           ||:  | | ||
Db        269 RSNPEPTGYNW------STTMGPLPPFAVAQGAQLLIRPVDKPINTTL 310
```

RESULT 9
I52590
m33-B isoform - mouse
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I52590
R;Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
Blood 83, 3188-3198, 1994
A;Title: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 anti
A;Reference number: I52590; MUID:94250900; PMID:8193354
A;Accession: I52590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-403 <RES>
A;Cross-references: GB:S71345; NID:g551352; PIDN:AAB30842.1; PID:g551353

Query Match 7.1%; Score 112.5; DB 2; Length 403;
Best Local Similarity 25.7%; Pred. No. 0.32;
Matches 73; Conservative 31; Mismatches 103; Indels 77; Gaps 13;

```
Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              :| ||      | ||  :||        : :  |: ::   |  | :| | :||    |
Db          1 MLWPL------PLFLLCAGSLAQ--DLEFQLVAPESVTVEEGLCVHVPCSVFYPSIKLTL 52

Qy         65 PDVRISW-RRG-HFHGQSFYSTRPPS--IHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                |  || |:|   |  |  :|  |   : |    |  |      :    | | : || |
Db         53 GPVTGSWLRKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDPQKHDCSLFIRDAQKNDT 112

Qy        121 SVYFCRV--ELDTRSSGRQQWQSIEGTKLSITQAV----TTTTQRPSSMTT--------- 165
              :|| ||  |   | | ::   |:  | ||| |  :     |      ||::|
Db        113 GMYFFRVVREPFVRYSYKKSQLSLHVTSLSRTPDIIIPGTLEAGYPSNLTCSVPWACEQG 172

Qy        166 -----TW------RLSSTTT-------------------------------TTGLRVT 181
                   :|       ||| ||                               |  | ||
Db        173 TPPTFSWMSTALTSLSSRTTDSSVLTFTPQPQDHGTKLTCLVTFSGAGVTVERTIQLNVT 232

Qy        182 QGKRRSDSWHISLETAVGVA-VAVTVLGIMILGLICLLRWRRRK 224
                |:|      :  ||| | | : :||: :: || :  : |||
Db        233 ---RKSGQMRELVLVAVGEATVKLLILGLCLVFLIVM--FCRRK 271
```

RESULT 10
S25758
Ig lambda chain - human
C;Species: Homo sapiens (man)

```
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25758
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25758
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57823; NID:g33745; PIDN:CAA40960.1; PID:g33746
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

  Query Match             6.9%;  Score 110;  DB 2;  Length 235;
  Best Local Similarity   24.2%;  Pred. No. 0.27;
  Matches   48;  Conservative   28;  Mismatches   70;  Indels   52;  Gaps    8;

Qy         26 GSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTR 85
              |:|      :|||  :| | | |: |  :       :: ||      | ::  |:|
Db         14 GTGSWAQSALTQPASVSGSPGQSITISCT-------GSSSDV------GGYNYVSWYQQH 60

Qy         86 PPSIHK----DYVNRL--FLNWTEGQKSG---FLRISNLQKQDQSVYFCRVELDTRSSGR 136
              |    |    |  ||     |   | |||    | || || :|:: |:|     |  :
Db         61 PGKAPKLMIYDVTNRPSGVSNRFSGSKSGNTASLTISGLQPEDEADYYC-----TSKTSS 115

Qy        137 QQWQSIEGTKLSI---TQAVTTTTQRPSS----------------------MTTTWRLSS 171
                :    |||:|:    :|  | | | |                     :|  |:
Db        116 SFYVFGTGTKVSVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADG 175

Qy        172 TTTTTGLRVTQGKRRSDS 189
              :    |:  |:  ::|::
Db        176 SPVKAGVETTKPSKQSNN 193


RESULT 11
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N;Alternate names: B-cell membrane protein CD22
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0371; I56171
R;Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A;Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell intera
A;Reference number: JH0371; MUID:91086838; PMID:1985119
A;Accession: JH0371
A;Molecule type: mRNA
A;Residues: 1-847 <WIL1>
A;Cross-references: UNIPROT:O60926; GB:X59350; NID:g36090; PIDN:CAA42006.1; PID:g36091
A;Experimental source: B lymphocyte
A;Note: the authors translated the codon AAT for residue 358 as Met
R;Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A;Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A;Reference number: I56171; MUID:93267103; PMID:8496602
A;Accession: I56171
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <WIL2>
A;Cross-references: GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:g3184492
C;Genetics:
A;Gene: GDB:CD22
A;Cross-references: GDB:127545; OMIM:107266
A;Map position: 19q13.1-19q13.1
A;Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphopro
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F;346-398/Domain: immunoglobulin homology <IMM1>
F;609-661/Domain: immunoglobulin homology <IMM2>
F;688-706/Domain: transmembrane #status predicted <TRA>
F;67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (coval
F;764,789/Binding site: phosphate (Thr) (covalent) #status predicted

  Query Match             6.9%;  Score 110;  DB 2;  Length 847;
  Best Local Similarity   22.1%;  Pred. No. 1.2;
  Matches   63;  Conservative   40;  Mismatches  116;  Indels   66;  Gaps   10;

Qy         30 SYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGH--FHGQSFYST--- 84
              ||   |      :||   ::|:    | |  |      |:|    |     |:|  |
Db        568 SYSCWVNNSIGQTASKAWTLEV---LYAPRRL------RVSMSPGDQVMEGKSATLTCES 618

Qy         85 --RPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSI 142
                ||  |  : :  : | :    |  ||:  :: |    |:|:    | | |: :
Db        619 DANPPVSHYTWFD--WNNQSLPHHSQKLRLEPVKVQHSGAYWCQ---GTNSVGKGR---- 669

Qy        143 EGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGKRRSDSWHISLETAVGVAV 202
                                  |  :|  :  :  | | ||                |||:
Db        670 ------------------SPLSTLTVYYSPETIGRRV---------------AVGLGS 694

Qy        203 AVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYENIRNEGQNTDPKLNP 262
               : :| : | ||    ||:| : ||  :  :  :  |   ::      :|| ::    ||
Db        695 CLAILILAICGLKLQRRWKRTQSQQGLQENSSGQSFFVRNKKVRRAPLSEGPHSLGCYNP 754

Qy        263 -KDDGIVYASLALSSSTSPR-----APPSHRPLKSPQNETLYSVL 301
              :||| | :|       ||      :    || ::  :   || |
Db        755 MMEDGISYTTLRFPEMNIPRTGDAESSEMQRPPRTCDDTVTYSAL 799


RESULT 12
S25747
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25747
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25747
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57812; NID:g33723; PIDN:CAA40949.1; PID:g33724
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

  Query Match             6.9%;  Score 109.5;  DB 2;  Length 233;
  Best Local Similarity   23.0%;  Pred. No. 0.29;
  Matches   53;  Conservative   29;  Mismatches   59;  Indels   89;  Gaps   11;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||| ||           |  |||  ||:  :|||  :| : | :  |           |
Db          6 LLLGLL-----------SHCTGSVTSYV--LTQPPSVSVAPGKAARI-----------TC 41

Qy         65 PDVRISWRRGHFHGQS--------FY--STRPPSIHKDYVNRLFLNWTEGQKSG---FLR 111
                : |: :  |:: |          |  | ||  | : :          |  ||    |
Db         42 GGINIASKSVHWYQQKPGQAPVLVVYGDSDRPSGIPERF---------SGSNSGNTATLN 92

Qy        112 ISNLQKQDQSVYFCRVELDTRSSGRQQWQSIE-------GTKLSI----TQAVTTTTQRP 160
              || ::  |:: |:|:|           | |          ||||::      | : |   |
Db         93 ISRVEAGDEAAYYCQV-----------WDSSSDHVVFGGGTKLTVLGQPKAAPSVTLFPP 141

Qy        161 SS--------------------MTTTWRLSSTTTTTGLRVTQGKRRSDS 189
              ||                    :|  |:  |:    |:  |   ::|::
Db        142 SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN 191


RESULT 13
S49449
Ig lambda chain - duck
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
```

```
C;Accession: S49449
R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, October 1994
A;Description: cDNA sequence and organization of the immunoglobulin light chain gene of
A;Reference number: S49449
A;Accession: S49449
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <MAG>
A;Cross-references: EMBL:X82069; NID:g558548; PIDN:CAA57568.1; PID:g558549
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-106/Domain: immunoglobulin homology <IMM>

  Query Match             6.8%;  Score 108.5;  DB 2;  Length 230;
  Best Local Similarity   20.5%;  Pred. No. 0.34;
  Matches   48;  Conservative   36;  Mismatches   61;  Indels   89;  Gaps    8;

Qy          4 PLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIP---FSFYYPWE 60
              |||| :|              :  ||       :|||    | : | :|:|      |  | |
Db          5 PLLLAVL-------------AHTSGSLVQAALTQPASKSVNPGDTVQITCSGSSSDYGWF 51

Qy         61 LATAP---DVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSG---FLRISN 114
                |     | : ::           : ||  |   :           | |||    | |:
Db         52 QQKTPGSAPVTVIYQN---------NKRPSGIPSRF---------SGSKSGSTATLTITG 93

Qy        115 LQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQ---------------- 158
              :| :|::||:|                | : : : :  | || |
Db         94 VQAEDEAVYYC--------------GSYDSSYVGVFGAGTTLTVLGQPKVSPTVHVFPPS 139

Qy        159 -------------------RPSSMTTTWRLSSTTTTTGLRVTQGKRRSDSWHIS 193
                                 || :| ||::: :| ::|:  :  :|:|:| :::
Db        140 DEEISSQNKATLVCLMSDFYPSPVTVTWKVNGSTRSSGVETSASQRQSNSKYMA 193


RESULT 14
S14675
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: S14675; S12445
R;Vasicek, T.J.
submitted to the EMBL Data Library, February 1990
A;Reference number: S14675
A;Accession: S14675
A;Molecule type: DNA
A;Residues: 1-235 <VAS1>
A;Cross-references: UNIPROT:Q8WUK4; EMBL:X51754
R;Vasicek, T.J.; Leder, P.
J. Exp. Med. 172, 609-620, 1990
A;Title: Structure and expression of the human immunoglobulin lambda genes.
A;Reference number: S12440; MUID:90324881; PMID:2115572
A;Accession: S12445
A;Molecule type: DNA
A;Residues: 1-129 <VAS2>
A;Cross-references: EMBL:X51754
C;Genetics:
A;Introns: 16/1; 130/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

  Query Match             6.8%;  Score 108.5;  DB 2;  Length 235;
  Best Local Similarity   23.9%;  Pred. No. 0.35;
  Matches   53;  Conservative   31;  Mismatches   67;  Indels   71;  Gaps   11;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              |:| ||             : |:|      :|||    | |:| ||    |        |:
Db          6 LILTLL-------------TQGTGSWAQSALTQPPSASGSLGQSVTFSCS-------GTS 45

Qy         65 PDV----RISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQKSG---FLRI 112
                |:     :|| | |  |::     :  |: ||       ||        | |||    | :
Db         46 SDIGNYNYVSWYRQH-PGKAPKLMIYEVTKRPS---GVPNRF-----SGSKSGNTASLTV 96


Qy        113 SNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSI----TQAVTTTTQRPSS------ 162
              | || :|:: |:|     :  :|         ||:|::      | : |   |||
Db         97 SGLQAEDEADYYC-----SSYAGSNSLIFGGGTRLTVLGQPKAAPSVTLFPPSSEELQAN 151

Qy        163 --------------MTTTWRLSSTTTTTGLRVTQGKRRSDS 189
                           :|  |:  |:    |:  |   ::|::
Db        152 KATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN 193


RESULT 15
I49583
differentiation antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49583
R;Law, C.
J. Immunol. 151, 175-187, 1993
A;Title: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterizat
A;Reference number: I49583; MUID:93315834; PMID:8100843
A;Accession: I49583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-862 <RES>
A;Cross-references: UNIPROT:P35329; GB:L16928; NID:g348965; PIDN:AAA02562.1; PID:g348966
C;Genetics:
A;Gene: CD22

  Query Match             6.8%;  Score 108.5;  DB 2;  Length 862;
  Best Local Similarity   20.1%;  Pred. No. 1.6;
  Matches   60;  Conservative   39;  Mismatches  109;  Indels   91;  Gaps   10;

Qy         10 LPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRI 69
              | :|  |  |: | | |       | : |  : |       | |  | |  ::
Db        602 LQVLYAPRRLRVSISPGD------HVMEGKKATLSCESDANPPIS-QYTWFDSS------ 648

Qy         70 SWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVEL 129
                      ||  :|:                   |||   ||:  |: |    | |:
Db        649 --------GQDLHSS------------------GQK---LRLEPLEVQHTGSYRCKG-- 676

Qy        130 DTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGKRRSDS 189
                                |  : |    ||::|  :    :  | | ||
Db        677 --------------------TNGIGTGESPPSTLTVYY----SPETIGKRV--------- 703

Qy        190 WHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYENI 249
                    |:|:   :|:  : | |:     :|:: : ||  :  :  :  |   ::
Db        704 -------ALGLGFCLTICILAIWGMKIQKKWKQNRSQQGLQENSSGQSFFVRNKKARRTP 756

Qy        250 RNEGQNTDPKLNP-KDDGIVYASLALSSSTSPRA-----PPSHRPLKSPQNETLYSVLK 302
               :||  :    ||  || : || |     |     |     | :  |  :  :   |||::
Db        757 LSEGPQSQGCYNPAMDDTVSYAILRFPESDMHNAGDAGTPATQAPPPNNSDSVTYSVIQ 815


Search completed: June  1, 2005, 22:14:01
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 1, 2005, 22:02:25 ; Search time 43 Seconds
(without alignments)
526.015 Million cell updates/sec

Title: US-10-777-524-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLPLLLPPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1591	100.0	303	3	US-08-985-950-2	Sequence 2, Appli
2	1591	100.0	303	4	US-09-546-049-2	Sequence 2, Appli
3	1591	100.0	303	4	US-09-869-388-2	Sequence 2, Appli
4	1176.5	73.9	230	4	US-09-869-388-4	Sequence 4, Appli
5	973.5	61.2	226	4	US-09-869-388-10	Sequence 10, Appl
6	958	60.2	227	4	US-09-869-388-6	Sequence 6, Appli
7	934	58.7	238	4	US-09-149-476-485	Sequence 485, App
8	821	51.6	175	4	US-09-869-388-8	Sequence 8, Appli
9	517	32.5	101	4	US-09-149-476-754	Sequence 754, App
10	222	14.0	99	3	US-08-985-950-4	Sequence 4, Appli
11	222	14.0	99	4	US-09-546-049-4	Sequence 4, Appli
12	130.5	8.2	431	3	US-09-038-832-2	Sequence 2, Appli
13	130.5	8.2	431	3	US-09-038-832-4	Sequence 4, Appli
14	130.5	8.2	447	4	US-09-949-016-8211	Sequence 8211, Ap
15	119	7.5	341	4	US-09-336-536-29	Sequence 29, Appl
16	119	7.5	370	4	US-09-336-536-28	Sequence 28, Appl
17	114	7.2	390	2	US-08-979-424-1	Sequence 1, Appli
18	114	7.2	390	4	US-09-907-794A-39	Sequence 39, Appl
19	114	7.2	390	4	US-09-905-125A-39	Sequence 39, Appl
20	114	7.2	390	4	US-09-902-775A-39	Sequence 39, Appl
21	114	7.2	390	4	US-09-906-700-39	Sequence 39, Appl
22	114	7.2	390	4	US-09-903-603A-39	Sequence 39, Appl
23	114	7.2	390	4	US-09-904-920A-39	Sequence 39, Appl
24	114	7.2	390	4	US-09-909-064-39	Sequence 39, Appl
25	114	7.2	390	4	US-09-905-381A-39	Sequence 39, Appl
26	114	7.2	390	4	US-09-906-618-39	Sequence 39, Appl
27	114	7.2	417	4	US-09-949-016-6729	Sequence 6729, Ap
28	114	7.2	456	4	US-09-949-016-7564	Sequence 7564, Ap
29	113.5	7.1	319	1	US-08-597-495B-22	Sequence 22, Appl
30	113.5	7.1	319	3	US-09-068-051A-22	Sequence 22, Appl
31	113.5	7.1	319	4	US-09-336-536-67	Sequence 67, Appl
32	113.5	7.1	319	4	US-09-254-465A-6	Sequence 6, Appli
33	113.5	7.1	319	4	US-09-953-499-6	Sequence 6, Appli
34	113	7.1	316	4	US-09-397-243D-13	Sequence 13, Appl
35	111.5	7.0	306	4	US-09-369-247-63	Sequence 63, Appl
36	110.5	6.9	244	3	US-08-918-148-79	Sequence 79, Appl
37	110.5	6.9	244	4	US-09-138-091A-77	Sequence 77, Appl
38	110	6.9	300	2	US-08-661-052-4	Sequence 4, Appli
39	110	6.9	300	3	US-09-188-082-4	Sequence 4, Appli
40	110	6.9	300	3	US-09-364-088-4	Sequence 4, Appli
41	110	6.9	300	3	US-09-102-716-4	Sequence 4, Appli
42	110	6.9	501	2	US-08-408-095-31	Sequence 31, Appl
43	106.5	6.7	216	4	US-09-291-299A-9	Sequence 9, Appli
44	106.5	6.7	240	3	US-09-049-672A-11	Sequence 11, Appl
45	105	6.6	512	4	US-08-999-689A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-950-2

Query Match 100.0%; Score 1591; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;

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  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
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Db        301 LKA 303


RESULT 2
US-09-546-049-2
; Sequence 2, Application US/09546049
; Patent No. 6479638
;   GENERAL INFORMATION:
;        APPLICANT: Adema, Gosse Jan
;                   Meyaard, Linde
;                   Gorman, Daniel M.
;                   McClanahan, Terrill K.
;                   Zurawski, Sandra M.
;                   Zurawski, Gerard
;                   Lanier, Lewis L.
;                   Phillips Jr., Joseph H.
;        TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                            Related Reagents
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/546,049
;             FILING DATE: 10-Apr-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/985,950
;             FILING DATE: 05-DEC-1997
;             APPLICATION NUMBER: US 60/041,279
;             FILING DATE: 21-MARCH-1997
;             APPLICATION NUMBER: US 60/033,181
;             FILING DATE: 16-DEC-1996
;             APPLICATION NUMBER: US 60/032,252
;             FILING DATE: 06-DEC-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0670K
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650)852-9196
;             TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 303 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2

  Query Match            100.0%;  Score 1591;  DB 4;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-141;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 3
US-09-869-388-2
; Sequence 2, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/09/869,388
;  CURRENT FILING DATE:  2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 2
;   LENGTH: 303
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-869-388-2

  Query Match            100.0%;  Score 1591;  DB 4;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-141;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
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Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
                |||
Db        301 LKA 303


RESULT 4
US-09-869-388-4
; Sequence 4, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHC
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/09/869,388
;  CURRENT FILING DATE:  2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 4
;   LENGTH: 230
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-869-388-4

  Query Match             73.9%;  Score 1176.5;  DB 4;  Length 230;
  Best Local Similarity   75.9%;  Pred. No. 1.2e-102;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   73;  Gaps    1;

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Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
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Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
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Db        168 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 227

Qy        301 LKA 303
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Db        228 LKA 230


RESULT 5
US-09-869-388-10
; Sequence 10, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/09/869,388
;  CURRENT FILING DATE:  2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 10
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-869-388-10

  Query Match             61.2%;  Score 973.5;  DB 4;  Length 226;
  Best Local Similarity   82.5%;  Pred. No. 1.5e-83;
  Matches  188;  Conservative   14;  Mismatches   17;  Indels    9;  Gaps    2;

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Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
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Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 6
US-09-869-388-6
; Sequence 6, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/09/869,388
;  CURRENT FILING DATE:  2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 6
;   LENGTH: 227
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-869-388-6

  Query Match             60.2%;  Score 958;  DB 4;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 4.2e-82;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

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                ||||||||||  || |||||||  ||||||||||||||||||||||||||||||||||||||||
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Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                ||  |:|||||||||||||||||||||||||||||||||||:|||||||||:|:||
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Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
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Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221


RESULT 7
US-09-149-476-485
; Sequence 485, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
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Query Match 58.7%; Score 934; DB 4; Length 238;
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Matches 179; Conservative 13; Mismatches 18; Indels 8; Gaps 1;

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RESULT 8
US-09-869-388-8
; Sequence 8, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-8

Query Match 51.6%; Score 821; DB 4; Length 175;
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Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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RESULT 9
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; Sequence 754, Application US/09149476
; Patent No. 6420526
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
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; CURRENT APPLICATION NUMBER: US/09/149,476
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;  EARLIER APPLICATION NUMBER: 60/061,060
;  EARLIER FILING DATE: 1997-10-02

  Query Match             32.5%;  Score 517;  DB 4;  Length 101;
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Db         61 NRLFLNWTEGQESGFLRISNLRKEDQSVYFCRVELDTRRSG 101


RESULT 10
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; Sequence 4, Application US/08985950
; Patent No. 6140076
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  99 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-985-950-4

  Query Match             14.0%;  Score 222;  DB 3;  Length 99;
  Best Local Similarity   45.2%;  Pred. No. 2.1e-13;
  Matches   42;  Conservative   15;  Mismatches   30;  Indels    6;  Gaps    1;

Qy         19 LQPSGSTGSGPSYLY------GVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWR 72
              |  ||   :| |  |      || ||:  |   |||::||||||:||:||  | : |:|:
Db          7 LLSSGCLHAGNSERYNRKNGFGVNQPERCSGVQGGSIDIPFSFYFPWKLAKDPQMSIAWK 66

Qy         73 RGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ 105
                 |||:  |::  | ||: :  || ||||:||
Db         67 WKDFHGEVIYNSSLPFIHEHFKGRLILNWTQGQ 99


RESULT 11
US-09-546-049-4
; Sequence 4, Application US/09546049
; Patent No. 6479638
;  GENERAL INFORMATION:
;       APPLICANT: Adema, Gosse Jan
;                  Meyaard, Linde
;                  Gorman, Daniel M.
;                  McClanahan, Terrill K.
;                  Zurawski, Sandra M.
;                  Zurawski, Gerard
;                  Lanier, Lewis L.
;                  Phillips Jr., Joseph H.
;       TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                           Related Reagents
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DNAX Research Institute
;            STREET: 901 California Avenue
;            CITY: Palo Alto
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94304-1104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/546,049
;            FILING DATE: 10-Apr-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/985,950
;            FILING DATE: 05-DEC-1997
;            APPLICATION NUMBER: US 60/041,279
;            FILING DATE: 21-MARCH-1997
;            APPLICATION NUMBER: US 60/033,181
;            FILING DATE: 16-DEC-1996
;            APPLICATION NUMBER: US 60/032,252
;            FILING DATE: 06-DEC-1996
;       ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0670K
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650)852-9196
;             TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 99 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-546-049-4

  Query Match            14.0%;  Score 222;  DB 4;  Length 99;
  Best Local Similarity  45.2%;  Pred. No. 2.1e-13;
  Matches   42;  Conservative   15;  Mismatches   30;  Indels    6;  Gaps    1;

Qy         19 LQPSGSTGSGPSYLY------GVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWR 72
              |  ||   :| |  |      || ||:  |   |||::||||||:||:||  | : |:|:
Db          7 LLSSGCLHAGNSERYNRKNGFGVNQPERCSGVQGGSIDIPFSFYFPWKLAKDPQMSIAWK 66

Qy         73 RGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ 105
                 |||:  |::  | ||: :  || ||||:||
Db         67 WKDFHGEVIYNSSLPFIHEHFKGRLILNWTQGQ 99


RESULT 12
US-09-038-832-2
; Sequence 2, Application US/09038832
; Patent No. 6146845
;  GENERAL INFORMATION:
;    APPLICANT:  KIKLY, KRISTINE
;    APPLICANT:  ERICKSON-MILLER, CONNIE
;    TITLE OF INVENTION:  Sialoadhesin Family Member-2
;    TITLE OF INVENTION:  (SAF-2)
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,832
;      FILING DATE:  11-MAR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/041,886
;      FILING DATE:  02-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-50018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-038-832-2

  Query Match            8.2%;  Score 130.5;  DB 3;  Length 431;
  Best Local Similarity  22.6%;  Pred. No. 0.00067;
  Matches   83;  Conservative   45;  Mismatches  138;  Indels  101;  Gaps   14;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||| |||||     ::  |   |  ||  | :  ::   |  | :| || || :  |
Db          3 LLLLLLPLLWGTKGME--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSFSYPQDGWTD 58

Qy         65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ---------KSGFLRISN 114
              | |   | |    |   |   | : :   :|     |:|:           | | :
Db         59 SDPVHGYWFRA---GDRPYQDAPVATNNP--DREVQAETQGRFQLLGDIWSNDCSLSIRD 113

Qy        115 LQKQDQSVYFCRVE---------------------------------LDTRSSGRQQ-- 138
               :|:|:  || |:|                                 | |  ||  :
Db        114 ARKRDKGSYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNL 173

Qy        139 -----WQSIEGTKLSIT--------------QAVTTTTQRPSSMTTTWRLSSTTTTTGL 178
                  |   :||   |:              :| | | :|   |:    |   ||:
Db        174 TCSVPWACKQGTPPMISWIGASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV 233

Qy        179 RVTQGKRRSDS---WHISL---------ETAVGVAVAVTVLGIMILGLICL--------L 218
              |   |   |   |::::          ||:|   :::||    | |:|         |
Db        234 TTTSTVRLDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPARL 293

Qy        219 RWRRRKGQQRTKATTPAREPFQN-TEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSS 277
              | |      :    |:|      | |  ::|:||: |    | :    :  ||:| :
Db        294 SWTR-----GSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE 348

Qy        278 TSPRAPP 284
               :  : |
Db        349 GTGTSRP 355


RESULT 13
US-09-038-832-4
; Sequence 4, Application US/09038832
; Patent No. 6146845
;  GENERAL INFORMATION:
;    APPLICANT:  KIKLY, KRISTINE
;    APPLICANT:  ERICKSON-MILLER, CONNIE
;    TITLE OF INVENTION:  Sialoadhesin Family Member-2
;    TITLE OF INVENTION:  (SAF-2)
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,832
;      FILING DATE:  11-MAR-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/041,886
;      FILING DATE:  02-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-50018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-038-832-4

  Query Match             8.2%;  Score 130.5;  DB 3;  Length 431;
  Best Local Similarity   22.6%;  Pred. No. 0.00067;
  Matches   83;  Conservative   45;  Mismatches  138;  Indels  101;  Gaps   14;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||| |||||     ::  |     |  ||  | :   ::    |  | :| || || :  |
Db          3 LLLLLLPLLWGTKGME--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSFSYPQDGWTD 58

Qy         65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ---------KSGFLRISN 114
              |  |   | |     |   |   | : :    :|     |:|:              | | :
Db         59 SDPVHGYWFRA---GDRPYQDAPVATNNP--DREVQAETQGRFQLLGDIWSNDCSLSIRD 113

Qy        115 LQKQDQSVYFCRVE---------------------------------LDTRSSGRQQ-- 138
              :|:|:  || |:|                                 | |  ||  :
Db        114 ARKRDKGSYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNL 173

Qy        139 -----WQSIEGTKLSIT--------------QAVTTTTQRPSSMTTTWRLSSTTTTTGL 178
                  |   :||   |:                  :| | | :|    |:     |   ||:
Db        174 TCSVPWACKQGTPPMISWIGASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV 233

Qy        179 RVTQGKRRSDS---WHISL---------ETAVGVAVAVTVLGIMILGLICL--------L 218
                |   |   |   |::::          ||:|   :::||    | |:|         |
Db        234 TTTSTVRLDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPARL 293

Qy        219 RWRRRKGQQRTKATTPAREPFQN-TEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSS 277
              | |      :    |:|       | |  ::|:||: |    | :    :  ||:| :
Db        294 SWTR-----GSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE 348

Qy        278 TSPRAPP 284
              :  : |
Db        349 GTGTSRP 355


RESULT 14
US-09-949-016-8211
; Sequence 8211, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8211
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8211

  Query Match             8.2%;  Score 130.5;  DB 4;  Length 447;
  Best Local Similarity   22.6%;  Pred. No. 0.00071;
  Matches   83;  Conservative   45;  Mismatches  138;  Indels  101;  Gaps   14;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||| |||||     ::  |     |  ||  | :   ::    |  | :| || || :  |
Db         19 LLLLLLPLLWGTKGME--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSFSYPQDGWTD 74

Qy         65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ---------KSGFLRISN 114
              |  |   | |     |   |   | : :    :|     |:|:              | | :
Db         75 SDPVHGYWFRA---GDRPYQDAPVATNNP--DREVQAETQGRFQLLGDIWSNDCSLSIRD 129

Qy        115 LQKQDQSVYFCRVE---------------------------------LDTRSSGRQQ-- 138
              :|:|:  || |:|                                 | |  ||  :
Db        130 ARKRDKGSYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNL 189

Qy        139 -----WQSIEGTKLSIT--------------QAVTTTTQRPSSMTTTWRLSSTTTTTGL 178
                  |   :||   |:                  :| | | :|    |:     |   ||:
Db        190 TCSVPWACKQGTPPMISWIGASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV 249

Qy        179 RVTQGKRRSDS---WHISL---------ETAVGVAVAVTVLGIMILGLICL--------L 218
                |   |   |   |::::          ||:|   :::||    | |:|         |
Db        250 TTTSTVRLDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPARL 309

Qy        219 RWRRRKGQQRTKATTPAREPFQN-TEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSS 277
              | |      :    |:|       | |  ::|:||: |    | :    :  ||:| :
Db        310 SWTR-----GSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE 364

Qy        278 TSPRAPP 284
              :  : |
Db        365 GTGTSRP 371


RESULT 15
US-09-336-536-29
; Sequence 29, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
;  APPLICANT: Leiby, K.
;  APPLICANT: McKay, C.
;  APPLICANT: Bossone, S.
;  TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
;  FILE REFERENCE: 7853-144
;  CURRENT APPLICATION NUMBER: US/09/336,536
;  CURRENT FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-336-536-29

  Query Match             7.5%;  Score 119;  DB 4;  Length 341;
  Best Local Similarity   21.4%;  Pred. No. 0.0058;
  Matches   71;  Conservative   44;  Mismatches  127;  Indels   90;  Gaps   11;

Qy         10 LPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRI 69
              | | ||   ||       || |  | :    |   |     |:||  :: ::     |  :
Db          2 LQLHLPANRLQAVEEGESGASAWYTL----HREVSSSQPWEVPFVMWF-FKQKEKEDQVL 56

Qy         70 SWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVEL 129
              |:  |         :|  | :          | ::   ::  ||:  ||::|   | | | :
Db         57 SYING-------VTTSKPGVS--------LVYSMPSRNLSLRVEGLQEKDSGPYSCSVNV 101

Qy        130 DTRSSGRQQWQSIEGTKLSIT-----------------QAVTTTTQRPSSMTTT---W-- 167
               :  |: :  ||:  :|::                  || : | | |         |
Db        102 QDK-QGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWDR 160

Qy        168 ----------------------RLSSTTTTTGLRVTQGKRRSDSWHISLETAVGVAVAV 204
                                   |||:     :     :  :::|| : |   ||
Db        161 QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAAV 220

Qy        205 -------TVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYENIRNEGQNTD 257
                    |::|: :|  : ||  || |                    |||  :|: :
Db        221 VAEAVVGTLVGLGLLAGLVLLYHRRGKA---------------LEEPANDIKEDAIAPR 264

Qy        258 PKLNPKDDGIVYASLALSSSTSPRA-PPSHRP 288
                  ||    :  :  ||| || ||  | | |
Db        265 TLPWPKSSDTISKNGTLSSVTSARALRPPHGP 296
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Search completed: June 1, 2005, 22:14:50
Job time : 45 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 1, 2005, 22:00:25 ; Search time 173 Seconds
(without alignments)
896.879 Million cell updates/sec

Title: US-10-777-524-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLPLLLPPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1588	99.8	303	2	Q9UKJ1	Q9ukj1 homo sapien
2	997.5	62.7	226	2	Q8NHI1	Q8nhi1 homo sapien
3	958	60.2	227	2	Q9UKJ0	Q9ukj0 homo sapien
4	630	39.6	299	2	Q8BYA6	Q8bya6 mus musculu
5	144.5	9.1	823	1	AXL2_YEAST	P38928 saccharomyc
6	139	8.7	290	2	Q6UX24	Q6ux24 homo sapien
7	139	8.7	290	2	Q7Z6A6	Q7z6a6 homo sapien
8	136	8.5	290	2	Q8TDQ1	Q8tdq1 homo sapien
9	135.5	8.5	293	2	Q7Z7I5	Q7z7i5 homo sapien
10	130.5	8.2	499	1	SIL8_HUMAN	Q9nyz4 homo sapien
11	130	8.2	289	2	Q6QX36	Q6qx36 mus musculu
12	129.5	8.1	233	2	Q8TBC9	Q8tbc9 homo sapien
13	129.5	8.1	499	2	Q7Z728	Q7z728 homo sapien
14	123.5	7.8	328	2	Q6ZMC9	Q6zmc9 homo sapien
15	123.5	7.8	353	2	Q7SDQ5	Q7sdq5 neurospora
16	122.5	7.7	235	2	Q99M11	Q99m11 mus musculu
17	122	7.7	288	2	O46707	O46707 fugu rubrip
18	122	7.7	367	2	Q9GJE4	Q9gje4 fugu rubrip
19	120	7.5	236	2	Q6PIQ7	Q6piq7 homo sapien
20	119.5	7.5	434	2	Q872V2	Q872v2 neurospora
21	119	7.5	318	2	Q9IB03	Q9ib03 sphoeroides
22	117.5	7.4	235	2	Q6P2J1	Q6p2j1 homo sapien
23	117.5	7.4	366	2	O46705	O46705 fugu rubrip
24	116	7.3	417	1	PVR_CERAE	P32506 cercopithec
25	115.5	7.3	513	1	SHS1_MOUSE	P97797 m protein-t
26	115	7.2	367	2	O46706	O46706 fugu rubrip
27	114.5	7.2	235	2	Q6PJG0	Q6pjg0 homo sapien
28	114	7.2	390	2	Q96AP7	Q96ap7 homo sapien
29	114	7.2	390	2	Q96T50	Q96t50 homo sapien
30	114	7.2	417	1	PVR_HUMAN	P15151 homo sapien
31	113.5	7.1	319	1	A33_HUMAN	Q99795 homo sapien
32	113.5	7.1	387	2	Q64JA4	Q64ja4 pan troglod
33	113	7.1	401	2	Q08835	Q08835 cercopithec
34	113	7.1	718	2	O73675	O73675 xenopus lae
35	113	7.1	718	2	Q6PCK4	Q6pck4 xenopus lae
36	112.5	7.1	403	1	CD33_MOUSE	Q63994 mus musculu
37	112.5	7.1	700	2	Q8TG00	Q8tg00 aspergillus
38	112.5	7.1	1795	2	O76894	O76894 drosophila
39	112	7.0	233	2	Q6PJA3	Q6pja3 homo sapien
40	111.5	7.0	369	2	O46704	O46704 fugu rubrip
41	111.5	7.0	506	1	SHS1_BOVIN	O46631 bos taurus
42	111.5	7.0	509	1	SHS1_RAT	P97710 r protein-t
43	110	6.9	253	2	Q8UZE2	Q8uze2 cercopithec
44	109.5	6.9	233	2	Q8N5F4	Q8n5f4 homo sapien
45	109.5	6.9	1225	2	Q6GP61	Q6gp61 xenopus lae

ALIGNMENTS

RESULT 1
Q9UKJ1
ID Q9UKJ1 PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibitory receptor PILRalpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
RT bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
RT paired with the truncated counterpart PILRbeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -.
DR Genew; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 303 AA; 33877 MW; 0410ADFC7E80928B CRC64;

Query Match 99.8%; Score 1588; DB 2; Length 303;
Best Local Similarity 99.7%; Pred. No. 5.6e-124;
Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
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Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPKAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 2
Q8NHI1
ID   Q8NHI1      PRELIMINARY;      PRT;   226 AA.
AC   Q8NHI1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PILRA protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017812; AAH17812.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   226 AA;  25478 MW;  5938181797733A30 CRC64;

  Query Match           62.7%;  Score 997.5;  DB 2;  Length 226;
  Best Local Similarity   67.8%;  Pred. No. 5.7e-75;
  Matches  196;  Conservative    6;  Mismatches   10;  Indels   77;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151
              |||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
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Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPL 289
              ||||||||||||||||||||||    :: : : |   ||: ||   |:
Db        168 NTEEPYENIRNEGQNTDPKLNPK----LHLTQSTSQPPSPQEPPERDPV 212


RESULT 3
Q9UKJ0
ID   Q9UKJ0      PRELIMINARY;      PRT;   227 AA.
AC   Q9UKJ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Activating receptor PILRbeta (Hypothetical protein DKFZp434O079).
GN   Name=DKFZp434O079;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA   Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT   "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
RT   bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
RT   paired with the truncated counterpart PILRbeta.";
RL   J. Biol. Chem. 275:4467-4474(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RG   The German cDNA Consortium;
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF161081; AAD52965.1; -.
DR   EMBL; AL834336; CAH10711.1; -.
DR   IntAct; Q9UKJ0; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein; Receptor.
SQ   SEQUENCE   227 AA;  25542 MW;  7FF960C60AB7EF09 CRC64;

  Query Match           60.2%;  Score 958;  DB 2;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 1.1e-71;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221


RESULT 4
Q8BYA6
ID   Q8BYA6      PRELIMINARY;      PRT;   299 AA.
AC   Q8BYA6;
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DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A630007P20 product:weakly similar to INHIBITORY
DE   RECEPTOR PILRALPHA.
GN   Name=Pilra; Synonyms=AV021745;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK041413; BAC30935.1; -.
DR   MGD; MGI:2450529; Pilra.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Receptor.
SQ   SEQUENCE   299 AA;  32992 MW;  C1158DC3E1B3F74F CRC64;

  Query Match             39.6%;  Score 630;  DB 2;  Length 299;
  Best Local Similarity   44.4%;  Pred. No. 3.2e-44;
  Matches  136;  Conservative   56;  Mismatches   96;  Indels   18;  Gaps    6;

Qy          5 LLLPLLPLLLP-------PAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYY 57
              ::| : |: :|        |:|  |  |  |     :|| ||:  |   |||::||||||:
Db          4 VVLSMFPVTVPCSGFRVSPSF--PGNSERSNRKNGFGVNQPESCSGVQGGSIDIPFSFYF 61

Qy         58 PWELATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQK 117
              ||:||  | : |:||   |||:  |::  | ||: :  || ||||:|| || ||| ||::
Db         62 PWKLAKDPQMSIAWRWKDFHGEFIYNSSLPFIHEHFKGRLILNWTQGQTSGVLRILNLKE 121

Qy        118 QDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTG 177
               ||: || || | | : | | |||| ||:|::|  |  | |  ||:       ::|:  |
Db        122 SDQTRYFGRVFLQT-TEGIQFWQSIPGTQLNVTNATCTPTTLPST------TAATSAHTQ 174

Qy        178 LRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPARE 237
               :|: |  ::   : |:| ||:| |  |  : :||||  | |:||:  |:|||  ||||
Db        175 NDITEVK-SANIGGLDLQTTVGLATAAAVFLVGVLGLIVFLWWKRRRQGQKTKAEIPARE 233

Qy        238 PFQNTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETL 297
              | : | | :|:: :|||  ||| ||||: |||||::||| |||   |:     :|| ||:
Db        234 PLE-TSEKHESVGHEGQCMDPKENPKDNNIVYASISLSSPTSPGTAPNLPVHGNPQEETV 292

Qy        298 YSVLKA 303
              ||::||
Db        293 YSIVKA 298


RESULT 5
AXL2_YEAST
ID   AXL2_YEAST     STANDARD;      PRT;   823 AA.
AC   P38928; Q96VY8;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   AXL2 protein precursor (SRO4 protein).
GN   Name=AXL2; Synonyms=REV7, SRO4; OrderedLocusNames=YIL140W;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Roemer T., Madden K., Chang J., Snyder M.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97313266; PubMed=9169870;
RA   Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA   Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA   Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA   Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA   Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL   Nature 387:84-87(1997).
RN   [3]
RP   SEQUENCE OF 1-775 FROM N.A.
RA   Mathew P.W.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 80-823 FROM N.A.
RA   Torpey L.E., Gibbs P.E.M., Nelson J., Lawrence C.W.;
RL   Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   INTERACTION WITH BUD5.
RX   PubMed=11313501; DOI=10.1126/science.1060360;
```

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RA   Kang P.J., Sanson A., Lee B., Park H.-O.;
RT   "A GDP/GTP exchange factor involved in linking a spatial landmark to
RT   cell polarity.";
RL   Science 292:1376-1378(2001).
CC   -!- FUNCTION: Required for axial budding pattern.
CC   -!- SUBUNIT: Interacts with BUD5.
CC   -!- SUBCELLULAR LOCATION: Must be delivered to the plasma membrane via
CC       the secretory pathway. Once anchored in the plasma membrane, it
CC       may recruit additional components to the incipient bud site.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U49845; AAA98666.1; -.
DR   EMBL; Z38059; CAA86138.1; -.
DR   EMBL; AF395906; AAK83884.1; -.
DR   EMBL; U07228; AAA67919.1; -.
DR   PIR; S48394; S48394.
DR   GermOnline; 139675; -.
DR   SGD; S000001402; AXL2.
DR   InterPro; IPR006644; Cadg.
DR   InterPro; IPR008009; He_PIG.
DR   Pfam; PF05345; He_PIG; 1.
DR   SMART; SM00736; CADG; 4.
KW   Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     22       Potential.
FT   CHAIN        23    823       AXL2 protein.
FT   TRANSMEM    509    529       Potential.
FT   CARBOHYD     41     41       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     50     50       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    117    117       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    163    163       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    260    260       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    266    266       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    304    304       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    359    359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    382    382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    389    389       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    403    403       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    447    447       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    451    451       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    495    495       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    595    595       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    649    649       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    663    663       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    737    737       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    803    803       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   823 AA;  90783 MW;  350D79758BF30771 CRC64;

  Query Match             9.1%;  Score 144.5;  DB 1;  Length 823;
  Best Local Similarity  24.7%;  Pred. No. 0.0031;
  Matches   72;  Conservative   45;  Mismatches   96;  Indels   79;  Gaps   16;

Qy         25 TGSGPSYLYGV-TQPKHLSASM---GGSVEIPFSFYYPWELATAPDV-------RISWRR 73
              :|| |  | |  : | : | |:    | |      |: :|: :  |:         |:  |
Db        308 SGSVPDELLGKNSNPANFSVSIYDTYGDV-----IYFNFEVVSTTDLFAISSLPNINATR 362

Qy         74 GHFHGQSFYSTRPPSIHKDYVNR----LFLN------WTEGQKS----------GFLRIS 113
              | :    |     ||   ||||      | |      | : | |           | ::|
Db        363 GEWFSYYFL----PSQFTDYVNTNVSLEFTNSSQDHDWVKFQSSNLTLAGEVPKNFDKLS 418

Qy        114 -----NLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTQRPSSMTTTWR 168
                  |   | | :||  : :|:: :      :   |: |     :|:|   :| | | :
Db        419 LGLKANQGSQSQELYFNIIGMDSKITHSNHSANATSTRSS---HHSTSTSSYTSSTYTAK 475

Qy        169 LSSTT---TTTGLRVTQGKRRSDSWHISLETAVGVAVAVTV-LGIMILGLIC-LLRWRRR 223
```

```
              :|||:   |::         :: | :   : || :|  | : ||:::: ||| |: ||||
Db        476 ISSTSAAATSSAPAALPAANKTSSHN---KKAVAIACGVAIPLGVILVALICFLIFWRRR 532

Qy        224 KGQQRTK----------ATTPAREPFQNTEEPYENIRNEGQNTDPKLNPKDD 265
              :    :           || :| |             :|  |  || ||
Db        533 RENPDDENLPHAISGPDLNNPANKPNQ------------ENATPLNNPFDD 571


RESULT 6
Q6UX24
ID   Q6UX24      PRELIMINARY;      PRT;   290 AA.
AC   Q6UX24;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PIGR.
GN   ORFNames=UNQ3105;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358545; AAQ88909.1; -.
DR   InterPro; IPR001986; EPSP_synth.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   290 AA;  32335 MW;  B3D84A6B417AB941 CRC64;

  Query Match             8.7%;  Score 139;  DB 2;  Length 290;
  Best Local Similarity  23.7%;  Pred. No. 0.0024;
  Matches   78;  Conservative   49;  Mismatches  126;  Indels   76;  Gaps   16;

Qy          7 LPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPD 66
              :||| | |   :|      || |    :| |  ::    ||: :   :   ||
Db          1 MPLLTLYLLLFWL-------SGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLK-- 51

Qy         67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                 | ||          :     :: | |  ::  : ||:    ::  :| | |   |:
Db         52 ---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYW 107

Qy        125 CRVELDTRSSGRQQWQSIEGTKLSITQAVTTTQRPSSMTTTWRLSSTTTTTGLRVTQGK 184
              | :|                 |  | :|  ||      |: :|     ||: | ||
Db        108 CGIEK-------------TGNDLGVTVQVTID---PAPVTQE-ETSSSPTLTG------- 143

Qy        185 RRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAR--EPFQNT 242
                |: |  |: :| : :  |:| :::|     || ||  | ||:     :| :  :| :
Db        144 HHLDNRHKLLKLSVLLPLIFTIL-LLLLVAASLLAWRMMKYQQKAAGMSPEQVLQPLEG- 201

Qy        243 EEPYENIRNEGQNTDP-----KLN-----------------PKDDGIVYASLALSSSTSP 280
              :  | ::  :   | |     ||:                 ||:| | |||| | :
Db        202 DLCYADLTLQLAGTSPRKATTKLSSAQVDQVEVEYVTMASLPKED-ISYASLTLGA--ED 258

Qy        281 RAP--------PSHRPLKSPQNETLYSVL 301
              : |         || | : |:  | || :
Db        259 QEPTYCNMGHLSSHLPGRGPEEPTEYSTI 287
```

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RESULT 7
Q7Z6A6
ID   Q7Z6A6      PRELIMINARY;      PRT;   290 AA.
AC   Q7Z6A6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Inhibitory receptor IREM1.
GN   Name=IREM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY303545; AAP57942.1; -.
DR   HSSP; O95944; 1HKF.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001986; EPSP_synth.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   290 AA;  32354 MW;  E9D84A6B417AA99B CRC64;

  Query Match             8.7%;  Score 139;  DB 2;  Length 290;
  Best Local Similarity   23.7%;  Pred. No. 0.0024;
  Matches   78;  Conservative   49;  Mismatches  126;  Indels   76;  Gaps   16;

Qy          7 LPLLPLLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPD 66
              :||| | |   :|       || |    :| |  ::    ||: :   :   ||
Db          1 MPLLTLYLLLFWL-------SGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLK-- 51

Qy         67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                | ||          :     :: | |  ::  : ||:    ::  :| | |   |:
Db         52 ---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYW 107

Qy        125 CRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGK 184
              | :|               |  | :|  ||     |: :|    ||: | ||
Db        108 CGIEK-------------TGNDLGVTVQVTID---PAPVTQE-ETSSSPTLTG------- 143

Qy        185 RRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAR--EPFQNT 242
                |: |  |: :| : :  |:| :::|    || ||  | ||:    :| :  :| :
Db        144 HHLDNRHKLLKLSVLLPLIFTIL-LLLLVAASLLAWRMMKYQQKAAGMSPEQVLQPLEG- 201

Qy        243 EEPYENIRNEGQNTDP-----KLN----------------PKDDGIVYASLALSSSTSP 280
              :  | ::  :   | |     ||:                  ||:| | |||| | :
Db        202 DLCYADLTLQLAGTSPRKATTKLSSAQVDQVEVEYVTMASLPKED-ISYASLTLGA--ED 258

Qy        281 RAP--------PSHRPLKSPQNETLYSVL 301
              : |         || | : |:  | || :
Db        259 QEPTYCNMGRLSSHLPGRGPEEPTEYSTI 287


RESULT 8
Q8TDQ1
ID   Q8TDQ1      PRELIMINARY;      PRT;   290 AA.
AC   Q8TDQ1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   NK inhibitory receptor.
GN   Name=NKIR;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15184070; DOI=10.1016/j.bbrc.2004.05.065;
RA   Sui L., Li N., Liu Q., Zhang W., Wan T., Wang B., Luo K., Sun H.,
RA   Cao X.;
RT   "IgSF13, a novel human inhibitory receptor of the immunoglobulin
RT   superfamily, is preferentially expressed in dendritic cells and
RT   monocytes.";
RL   Biochem. Biophys. Res. Commun. 319:920-928(2004).
DR   EMBL; AF251706; AAM19099.1; -.
DR   HSSP; O95944; 1HKF.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001986; EPSP_synth.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   290 AA;  32395 MW;  D14FC04A047AAD10 CRC64;

  Query Match             8.5%;  Score 136;  DB 2;  Length 290;
  Best Local Similarity   23.7%;  Pred. No. 0.0042;
  Matches   78;  Conservative   48;  Mismatches  127;  Indels   76;  Gaps   16;

Qy          7 LPLLPLLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPD 66
              :||| | |   :|       || |    :| |  ::    ||: :   :   ||
Db          1 MPLLTLYLLLFWL-------SGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLK-- 51

Qy         67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                | ||          :     :: | |  ::  : ||:    ::  :| | |   |:
Db         52 ---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYW 107

Qy        125 CRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGK 184
              | :|               |  | :|  ||     |: :|    ||  | ||
Db        108 CGIEK-------------TGNDLGVTVQVTID---PAPVTQE-ETSSFPTLTG------- 143

Qy        185 RRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAR--EPFQNT 242
                |: |  |: :| : :  |:| :::|    || ||  | ||:    :| :  :| :
Db        144 HHLDNRHKLLKLSVLLPLIFTIL-LLLLVAASLLAWRMMKYQQKAAGMSPEQVLQPLEG- 201

Qy        243 EEPYENIRNEGQNTDP-----KLN----------------PKDDGIVYASLALSSSTSP 280
              :  | ::  :   | |     ||:                  ||:| | |||| | :
Db        202 DLCYADLTLQLAGTSPRKATTKLSSAQVDQVEVEYVTMASLPKED-ISYASLTLGA--ED 258

Qy        281 RAP--------PSHRPLKSPQNETLYSVL 301
              : |         || | : |:  | || :
Db        259 QEPTYCNMGHLSSHLPGRGPEEPTEYSTI 287


RESULT 9
Q7Z7I5
ID   Q7Z7I5      PRELIMINARY;      PRT;   293 AA.
AC   Q7Z7I5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immune receptor expressed on myeloid cells splice variant 1.
GN   Name=IREM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF375480; AAP42152.1; -.
DR   HSSP; O95944; 1HKF.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
```

```
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   293 AA;  32655 MW;  66EBEA2F8D3CF43E CRC64;

  Query Match             8.5%;  Score 135.5;  DB 2;  Length 293;
  Best Local Similarity   22.8%;  Pred. No. 0.0047;
  Matches   75;  Conservative   51;  Mismatches  128;  Indels   75;  Gaps   16;

Qy          7 LPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPD 66
              || | |      ::   :  | |   :| |  ::    ||: :   :   ||
Db          3 LPQLDL------MRVISAKSQGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLK-- 54

Qy         67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                | ||          :     :: | |  ::  : ||:    ::  :| | |   |:
Db         55 ---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYW 110

Qy        125 CRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGK 184
              | :|               |  | :|  ||     |: :|    :||: | ||
Db        111 CGIEK------------TGNDLGVTVQVTID---PAPVTQE-EISSSPTLTG------- 146

Qy        185 RRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAR--EPFQNT 242
              |: |  |: :| : :  |:| :::|    || ||  | ||:    :| :  :| :
Db        147 HHLDNRHKLLKLSVLLPLIFTIL-LLLLVAASLLAWRMMKYQQKAAGMSPEQVLQPLEG- 204

Qy        243 EEPYENIRNEGQNTDP-----KLN----------------PKDDGIVYASLALSSSTSP 280
              :  | ::  :   | |     ||:                ||:| | |||| | :
Db        205 DLCYADLTLQQAGTSPRKATTKLSSAQVDQVEVEYVTMASLPKED-ISYASLTLGA--ED 261

Qy        281 RAP--------PSHRPLKSPQNETLYSVL 301
              : |         || | : |:  | || :
Db        262 QEPTYCNMGHLSSHLPGRGPEEPTEYSTI 290


RESULT 10
SIL8_HUMAN
ID   SIL8_HUMAN     STANDARD;      PRT;   499 AA.
AC   Q9NYZ4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Sialic acid binding Ig-like lectin 8 precursor (Siglec-8)
DE   (Sialoadhesin family member-2) (SAF-2).
GN   Name=SIGLEC8; Synonyms=SAF2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=20549027; PubMed=11095983; DOI=10.1006/bbrc.2000.3866;
RA   Foussias G., Yousef G.M., Diamandis E.P.;
RT   "Molecular characterization of a siglec8 variant containing
RT   cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
RL   Biochem. Biophys. Res. Commun. 278:775-781(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RX   MEDLINE=20314554; PubMed=10856141; DOI=10.1067/mai.2000.107127;
RA   Kikly K.K., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.T.,
RA   D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,
RA   Murdock P.R., Tachimoto H., Schleimer R.P., White J.R.;
RT   "Identification of SAF-2, a novel siglec expressed on eosinophils,
RT   mast cells, and basophils.";
RL   J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Eosinophil;
RX   MEDLINE=20092847; PubMed=10625619; DOI=10.1074/jbc.275.2.861;
RA   Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.,
RA   Crocker P.R.;
RT   "Siglec-8. A novel eosinophil-specific member of the immunoglobulin
RT   superfamily.";
RL   J. Biol. Chem. 275:861-866(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Floyd H., Zhang J.Q., Crocker P.R.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC       dependent binding to cells. Preferentially binds to alpha2,3-
CC       linked sialic acid. Also binds to alpha2,6-linked sialic acid. The
CC       sialic acid recognition site may be masked by cis interactions
CC       with sialic acids on the same cell surface.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1; Synonyms=Long;
CC         IsoId=Q9NYZ4-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9NYZ4-2; Sequence=VSP_002559;
CC       Name=3;
CC         IsoId=Q9NYZ4-3; Sequence=VSP_002560;
CC   -!- TISSUE SPECIFICITY: Expressed specifically on eosinophils.
CC   -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC       as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC       motif is involved in modulation of cellular responses. The
CC       phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC       containing phosphatases.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC       (sialic acid binding Ig-like lectin) family.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF287892; AAG00573.1; -.
DR   EMBL; AF223403; AAF34702.1; -.
DR   EMBL; AF195092; AAF27622.1; -.
DR   EMBL; AF310234; AAK55140.1; -.
DR   HSSP; Q9Y286; 1O7S.
DR   Genew; HGNC:10877; SIGLEC8.
DR   MIM; 605639; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005529; F:sugar binding; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Alternative splicing; Cell adhesion; Glycoprotein;
KW   Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    499       Sialic acid binding Ig-like lectin 8.
FT   DOMAIN       17    363       Extracellular (Potential).
FT   TRANSMEM    364    384       Potential.
FT   DOMAIN      385    499       Cytoplasmic (Potential).
FT   DOMAIN       40    123       Ig-like V-type.
FT   DOMAIN      157    240       Ig-like C2-type 1.
FT   DOMAIN      246    344       Ig-like C2-type 2.
FT   SITE        445    450       ITIM motif.
FT   SITE        468    473       SLAM-like motif.
FT   DISULFID     42    181       By similarity.
FT   DISULFID     47    107       By similarity.
FT   DISULFID    175    224       By similarity.
FT   DISULFID    283    328       By similarity.
FT   CARBOHYD    172    172       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    267    267       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    152    245       ALTHRPDILILGTLESGHSRNLTCSVPWACKQGTPPMISWI
FT                                GASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV
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FT                                TTTSTVRLDVSY -> D (in isoform 2).
FT                                /FTId=VSP_002559.
FT   VARSPLIC    416    499       GPLTESWKDGNPLKKPPPAVAPSSGEEGELHYATLSFHKVK
FT                                PQDPQGQEATDSEYSEIKIHKRETAETQACLRNHNPSSKEV
FT                                RG -> VSDVGFSTPSIQPGHL (in isoform 3).
FT                                /FTId=VSP_002560.
SQ   SEQUENCE   499 AA;  54042 MW;  086EFF989B74123C CRC64;

  Query Match             8.2%;  Score 130.5;  DB 1;  Length 499;
  Best Local Similarity   22.6%;  Pred. No. 0.024;
  Matches   83;  Conservative   45;  Mismatches  138;  Indels  101;  Gaps   14;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              ||| |||||     ::  |    |  ||  | :   ::    |  | :| || || :  |
Db          3 LLLLLLPLLWGTKGME--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSFSYPQDGWTD 58

Qy         65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ---------KSGFLRISN 114
               | |   | |    |   |    | : :    :|      |:|:             | | :
Db         59 SDPVHGYWFRA---GDRPYQDAPVATNNP--DREVQAETQGRFQLLGDIWSNDCSLSIRD 113

Qy        115 LQKQDQSVYFCRVE---------------------------------LDTRSSGRQQ-- 138
               :|:|:  || |:|                                 | |  ||  :
Db        114 ARKRDKGSYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNL 173

Qy        139 -----WQSIEGTKLSIT---------------QAVTTTTQRPSSMTTTWRLSSTTTTTGL 178
                    |   :||   |:                :| | | :|    |:    |   ||:
Db        174 TCSVPWACKQGTPPMISWIGASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV 233

Qy        179 RVTQGKRRSDS---WHISL---------ETAVGVAVAVTVLGIMILGLICL--------L 218
                |   |   |   |::::          ||:|   :::||    | |:|          |
Db        234 TTTSTVRLDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPARL 293

Qy        219 RWRRRKGQQRTKATTPAREPFQN-TEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSS 277
              | |      :    |:|       | |  ::|:||: |    | :    :  ||:| :
Db        294 SWTR-----GSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE 348

Qy        278 TSPRAPP 284
              :  : |
Db        349 GTGTSRP 355


RESULT 11
Q6QX36
ID   Q6QX36      PRELIMINARY;      PRT;   289 AA.
AC   Q6QX36;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CRKD-binding protein.
GN   Name=Crkr;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD1;
RA   Corbit K.C., Kuo A.C., Chen F., Crabtree G.R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY522648; AAS13453.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   289 AA;  32831 MW;  9B97CA7C01B6F17D CRC64;

  Query Match             8.2%;  Score 130;  DB 2;  Length 289;
  Best Local Similarity   22.4%;  Pred. No. 0.013;
  Matches   69;  Conservative   41;  Mismatches  114;  Indels   84;  Gaps   12;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
              || |:| |||       |||           :|: | |  | :| :
Db          8 LLSPVLLLLL------ASGS---------WTQKPELLRAQEGETVSL------------ 39

Qy         65 PDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFL------------RI 112
                    |    :|       :      | :  ||::    :|  ||            :
Db         40 ----TCWYDSLYHSDEKIWCK----QIDNLCYLFVS-KSAEKPRFLIQQSSRFNFPTVTM 90

Qy        113 SNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSST 172
              : |:  |  :| | : ::||                :   :::     : || ||||| ::
Db         91 TKLKMSDSGIYHCGIAVNTR--------------IIYLRSIHLVVSKASS-TTTWRTTTL 135

Qy        173 TTTTGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKAT 232
              :|      :    |  |         || ||| :|   :: :|  ||  |||
Db        136 ASTHSPVTNRSFPDSPMWK---AIVAGVVVAVLLLLTFVILVILYLRKARRKALNVQNQC 192

Qy        233 TPAREPFQNTEEPYENIRNEGQNTDPKLNPKDDG-IVYASL----------ALSSSTSPR 281
              |  | | : :|   :   :  :::      | | | ||||          :: |:| |
Db        193 HPIYEDFSDQKEETTSFNQQTHSSE------DTGTICYASLIHLNRVNPQDSIYSNTQPY 246

Qy        282 APPSHRPL 289
              || ||
Db        247 PKPSPDPL 254


RESULT 12
Q8TBC9
ID   Q8TBC9      PRELIMINARY;      PRT;   233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022823; AAH22823.1; -.
DR   PIR; S12442; S12442.
DR   PIR; S30525; S30525.
DR   PIR; S30526; S30526.
DR   HSSP; P01842; 1LIL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
```

```
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24867 MW;  367411BFD6F4DF92 CRC64;

  Query Match             8.1%;  Score 129.5;  DB 2;  Length 233;
  Best Local Similarity   24.2%;  Pred. No. 0.011;
  Matches   54;  Conservative   32;  Mismatches   64;  Indels   73;  Gaps   10;

Qy          4 PLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEI---------PFS 54
              ||||||| |               |||  |  | :|||  :| | | :  |          ::
Db          5 PLLLPLLTL-----------CTGSEAS--YELTQPPSVSVSPGQTARITCSGDALPKQYA 51

Qy         55 FYYPWELATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSG---FLR 111
              ::|  :   || | : ::          : ||  | : :         |  ||    |
Db         52 YWYQQKPGQAP-VLVIYKD---------NERPSGIPERF---------SGSSSGTTVTLT 92

Qy        112 ISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSI----TQAVTTTTQRPSS----- 162
              || :| :|:: |:|:    :  |     |    ||||::      | : |   |||
Db         93 ISGVQAEDEADYYCQ----SADSSGTYWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQA 148

Qy        163 ----------------MTTTWRLSSTTTTTGLRVTQGKRRSDS 189
                           :|  |:  |:    |:  |   ::|::
Db        149 NKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN 191


RESULT 13
Q7Z728
ID   Q7Z728      PRELIMINARY;      PRT;   499 AA.
AC   Q7Z728;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053319; AAH53319.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   499 AA;  54052 MW;  CA32FEF7A88A7D3D CRC64;

  Query Match             8.1%;  Score 129.5;  DB 2;  Length 499;
  Best Local Similarity   22.6%;  Pred. No. 0.029;
  Matches   83;  Conservative   45;  Mismatches  138;  Indels  101;  Gaps   14;

Qy          5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSPYYPWELATA 64
              ||| |||||     ::  |    |  ||  | :   ::    |  | :| || || :  |
Db          3 LLLLLLPLLWGTKGME--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSFSYPQDGWTD 58

Qy         65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ---------KSGFLRISN 114
               | |   | |     |   |   | : :    :|      |:|:             | | :
Db         59 SDPVHGYWFRA---GDRPYQDAPVATNNP--DREVQAETQGRFQLLGDIWSNDCSLSIRD 113

Qy        115 LQKQDQSVYFCRVE---------------------------------LDTRSSGRQQ-- 138
               :|:|:  || |:|                                 | |  ||  :
Db        114 ARKRDKGSYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHPRNL 173

Qy        139 -----WQSIEGTKLSIT--------------QAVTTTTQRPSSMTTTWRLSSTTTTTGL 178
                   |   :||   |:                :| | | :|    |:    |   ||:
Db        174 TCSVPWACKQGTPPMISWIGASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV 233

Qy        179 RVTQGKRRSDS---WHISL---------ETAVGVAVAVTVLGIMILGLICL--------L 218
                 |   |   |   |::::          ||:|   :::||    | |:|         |
Db        234 TTTSTVRLDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPARL 293

Qy        219 RWRRRKGQQRTKATTPAREPFQN-TEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSS 277
                | |      :    |:|       | |  ::|:||: |    | :    :  ||:| :
Db        294 SWTR-----GSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE 348

Qy        278 TSPRAPP 284
                :  : |
Db        349 GTGTSRP 355


RESULT 14
Q6ZMC9
ID   Q6ZMC9      PRELIMINARY;      PRT;   328 AA.
AC   Q6ZMC9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ23996.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA   Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK172835; BAD18800.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   328 AA;  35652 MW;  534D6D2E76F04C8B CRC64;

  Query Match             7.8%;  Score 123.5;  DB 2;  Length 328;
  Best Local Similarity   20.3%;  Pred. No. 0.054;
  Matches   72;  Conservative   42;  Mismatches  123;  Indels  117;  Gaps   15;

Qy         12 LLLPPAFLQPSGS----------------TGSGPSYLYGVTQPKHLSASMGGSVEIPFSF 55
              ||   |:: |:||                | |:  : :  |  :||  | :  :| :|
Db          7 LLACLAWVLPTGSFVRTKIDTTENLLNTEVHSSPAQRWSMQVPPEVSAEAGDAAVLPCTF 66

Qy         56 YYPWELATAPDVRISWRRGH-FHGQSFYSTRPP----------SIHKDYVNRLFLNWTEG 104
               :|      |   | || |  : |   :                |:|  :  ||  |
Db         67 THPHRHYDGPLTAI-WRAGEPYAGPQVFRCAAARGSELCQTALSLHGRF--RLLGNPRRN 123
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Qy        105 QKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQA------------ 152
Db        124 DLS--LRVERLALADDRRYFCRVEF--AGDVHDRYESRHGVRLHVTAAPRIVNISVLPSP 179

Qy        153 -------VTTTTQRPSSMT----------------------TTWRLSSTT-----TTTG 177
Db        180 AHAFRALCTAEGEPPPALAWSGPALGNSLAAVRSPREGHGHLVTAELPALTHDGRYTCTA 239

Qy        178 LRVTQGKRRSDSWHISLETAVGVAVAVTVLG------IMILGLICLLRWRRRKGQQRTKA 231
Db        240 AN-SLGRSEASVYLFRFHGASGASTVALLLGALGFKALLLLGVLA-ARAARRRPEHLDTP 297

Qy        232 TTPAREPFQNTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPS 285
Db        298 DTPPRS--QAQESNYENL-------------------------SQMNPRSPPA 323


RESULT 15
Q7SDQ5
ID   Q7SDQ5      PRELIMINARY;      PRT;   353 AA.
AC   Q7SDQ5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Predicted protein (Hypothetical protein B10D6.180).
GN   Name=NCU02847.1; Synonyms=B10D6.180;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   German Neurospora genome project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000046; EAA34901.1; -.
DR   EMBL; BX842624; CAE76234.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   353 AA;  36684 MW;  CF9D98A22429891A CRC64;

  Query Match             7.8%;  Score 123.5;  DB 2;  Length 353;
  Best Local Similarity   23.1%;  Pred. No. 0.059;
  Matches   66;  Conservative   32;  Mismatches   81;  Indels  107;  Gaps   12;

Qy         26 GSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTR 85
Db        146 GSDPADL----------ATMTISDDKDFMFY-------APLIQINWQS---------SDR 179

Qy         86 PPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGT 145
Db        180 P--------------TETVFSGTVSLS------------VDVDTMST--------LAT 203

Qy        146 KLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRVTQGKRRSDSWH-ISLETA--VGVAV 202
Db        204 AGDAPAGVTSRVGFPSQSVVLVGSQGSNKPTG--ASEGNKEEDGVKPVSLSTGFKVGMAV 261

Qy        203 AVTVLGIMILGLICLLRWRRRKGQQR---------TKATTPAREPFQNTE---------- 243
Db        262 AGGVLAVAIVAIIFICAWRRRKQQMEEEEFDRMYGMKDVGPSTADFRNEEIPGWHRGPTR 321

Qy        244 ----EPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPS 285
Db        322 RQPPAPVDPFRSDGES----------------ELMAPPAPYHPPS 350


Search completed: June  1, 2005, 22:13:16
Job time : 176 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 1, 2005, 21:56:35 ; Search time 162 Seconds
(without alignments)
723.385 Million cell updates/sec

Title: US-10-777-524-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLPLLLPPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1591	100.0	303	2	AAW62772	Aaw62772 Human imm
2	1591	100.0	303	3	AAB07443	Aab07443 A human m
3	1588	99.8	303	8	ADP25129	Adp25129 PRO polyp
4	1176.5	73.9	230	3	AAB07444	Aab07444 A human m
5	1171.5	73.6	230	7	ADE95578	Ade95578 Human NOV
6	1010.5	63.5	206	7	ADE95580	Ade95580 Human NOV
7	973.5	61.2	226	2	AAY08015	Aay08015 Human LSP
8	973.5	61.2	226	3	AAB07447	Aab07447 A human m
9	967.5	60.8	226	2	AAW80407	Aaw80407 A secrete
10	967.5	60.8	226	5	ABP61825	Abp61825 Human pol
11	958	60.2	227	3	AAB07445	Aab07445 A human m
12	958	60.2	227	6	ABU89824	Abu89824 TNF-recep
13	958	60.2	291	2	AAW63682	Aaw63682 Human sec
14	958	60.2	326	4	ABB12010	Abb12010 Human sec
15	945	59.4	227	3	AAY87230	Aay87230 Human sig
16	934	58.7	238	5	ABG95345	Abg95345 Human nov
17	934	58.7	238	6	ABO34539	Abo34539 Region of
18	934	58.7	238	7	ADI23200	Adi23200 Novel hum
19	934	58.7	238	8	ADH74202	Adh74202 Human sec
20	927.5	58.3	228	8	ADK98565	Adk98565 Human imm
21	821	51.6	175	3	AAB07446	Aab07446 A human m
22	808	50.8	1012	4	ABG00509	Abg00509 Novel hum
23	808	50.8	1012	4	ABG16869	Abg16869 Novel hum
24	808	50.8	1012	4	ABG02851	Abg02851 Novel hum
25	808	50.8	1012	4	ABG21403	Abg21403 Novel hum
26	517	32.5	101	2	AAW75053	Aaw75053 Fragment
27	517	32.5	101	5	ABG95614	Abg95614 Human nov
28	517	32.5	101	6	ABO34808	Abo34808 Fragment
29	517	32.5	101	7	ADI23469	Adi23469 Novel hum
30	517	32.5	101	8	ADH74471	Adh74471 Human sec
31	411	25.8	224	5	ABB72387	Abb72387 Murine pr
32	405.5	25.5	212	7	ADE59537	Ade59537 Rat Prote
33	222	14.0	99	2	AAW62773	Aaw62773 Partial m
34	148.5	9.3	305	4	AAU14284	Aau14284 Human nov
35	146.5	9.2	305	4	AAU14520	Aau14520 Human nov
36	146.5	9.2	305	4	AAB66271	Aab66271 Human TAN
37	146.5	9.2	305	5	AAU08796	Aau08796 Human leu
38	146.5	9.2	305	5	AAO19216	Aao19216 Human sec
39	146.5	9.2	305	8	ADS11833	Ads11833 Human the
40	146.5	9.2	305	8	ADS11832	Ads11832 Human the
41	146.5	9.2	305	8	ADS11831	Ads11831 Human the
42	146.5	9.2	305	8	ADS10561	Ads10561 Human the
43	145.5	9.1	305	8	ADH80838	Adh80838 Human pol
44	139	8.7	290	4	AAB74712	Aab74712 Human mem
45	139	8.7	290	5	AAU83611	Aau83611 Human PRO

ALIGNMENTS

RESULT 1
AAW62772
ID AAW62772 standard; protein; 303 AA.
XX
AC AAW62772;
XX
DT 23-SEP-1998 (first entry)
XX
DE Human immunoglobulin receptor designated FDF03.
XX
KW Human; type I transmembrane protein; immunoglobulin-like domain; FDF03;
KW activated monocyte; YE01; KTE03; control; development; differentiation;
KW mammalian immune system; treatment; cancerous condition;
KW degenerative condition; autoimmune response; transplantation rejection;
KW graft versus host disease; inflammatory condition; detection; diagnosis;
KW drug screening.
XX
OS Homo sapiens.
XX
PN WO9824906-A2.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-US021101.
XX
PR 06-DEC-1996; 96US-0032252P.
PR 09-DEC-1996; 96US-00762187.
PR 16-DEC-1996; 96US-0033181P.
PR 21-MAR-1997; 97US-0041279P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Adema GJ, Meyaard L, Gorman DM, Mcclanahan TK, Zurawski SM;
PI Zurawski G, Lanier LL, Phillips JH;
XX
DR WPI; 1998-333325/29.
DR N-PSDB; AAV38987.
XX
PT New isolated activated monocyte cell gene(s) - used to develop products
PT for treating e.g. cancer, degenerative conditions, autoimmune responses,
PT transplant rejection or inflammatory conditions.
XX
PS Claim 1; Page 60-61; 104pp; English.
XX
CC The present sequence represents a human protein, FDF03, which is a type I
CC transmembrane protein comprising an extracellular portion characterised
CC by immunoglobulin-like domains, indicating that the protein is a receptor
CC member of the immunoglobulin superfamily. The FDF03 gene is found in

```
CC   activated monocytes. The specification also describes other proteins
CC   encoded by activated monocytes, which are designated YE01 and KTE03. The
CC   genes function in controlling development, differentiation, and/or
CC   physiology of the mammalian immune system. The products can be used for
CC   treating abnormal proliferation, regeneration, degeneration or atrophy.
CC   They can be used for treating e.g. cancerous conditions, degenerative
CC   conditions, autoimmune responses, transplantation rejection, graft versus
CC   host disease, or inflammatory conditions. The products can also be used
CC   for detection, diagnosis and drug screening
XX
SQ   Sequence 303 AA;

  Query Match            100.0%;  Score 1591;  DB 2;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-122;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 2
AAB07443
ID   AAB07443 standard; protein; 303 AA.
XX
AC   AAB07443;
XX
DT   20-OCT-2000  (first entry)
XX
DE   A human monocyte-derived protein FDF03.
XX
KW   Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
KW   FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
KW   tissue rejection; inflammation; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /note= "signal peptide"
FT   Protein         20. .303
FT                   /note= "mature protein"
XX
PN   WO200040721-A1.
XX
PD   13-JUL-2000.
XX
PF   29-DEC-1999;   99WO-US030004.
XX
PR   31-DEC-1998;   98US-00223919.
PR   31-DEC-1998;   98US-00224604.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bates E,  Fournier N,  Chaulus L,  Garrone P;
XX
DR   WPI; 2000-465984/40.
DR   N-PSDB; AAA58814.
XX
PT   Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT   diseases associated with changes in monocyte numbers, e.g. bacterial or
PT   viral infections.
XX
PS   Claim 1; Page 32-33; 45pp; English.
XX
CC   The present sequence represents a human monocyte-derived protein. The
CC   specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
CC   FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
CC   regulation, or development, of haematopoietic cells. Antibodies specific
CC   for antigenic components of the proteins can be used to detect the
CC   components in samples. The proteins can also be used to screen for
CC   candidate therapeutic agents. The monocyte-derived proteins and
CC   polynucleotides can be used for diagnosis of diseases related to an
CC   increase, or decrease, in the number of monocytes in a tissue or lymph
CC   system, such as monocyte hyperplasia, tissue or graft rejection,
CC   inflammation, or bacterial or viral infections. The proteins can also be
CC   used in the treatment of disorders associated with abnormal expression or
CC   signalling by a monocyte
XX
SQ   Sequence 303 AA;

  Query Match            100.0%;  Score 1591;  DB 3;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-122;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 3
ADP25129
ID   ADP25129 standard; protein; 303 AA.
XX
AC   ADP25129;
XX
DT   18-NOV-2004  (first entry)
XX
DE   PRO polypeptide SEQ ID NO:2307.
XX
KW   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW   osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW   antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS   Unidentified.
XX
```

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PN   WO2004041170-A2.
XX
PD   21-MAY-2004.
XX
PF   30-OCT-2003; 2003WO-US034312.
XX
PR   01-NOV-2002; 2002US-0423394P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Clark H,  Schoenfeld J,  Van Lookeren M,  Williams PM,  Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-419628/39.
DR   N-PSDB; ADP25128.
XX
PT   New PRO polypeptides and polynucleotides, useful for treating e.g.
PT   erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT   renal disease, or demyelinating diseases of the central or peripheral
PT   nervous system.
XX
PS   Claim 7; SEQ ID NO 2307; 2940pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid and the PRO
CC   polypeptide encoded by it. A protein of the invention has
CC   antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC   osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC   antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC   of the invention may have a use in gene therapy. The PRO polypeptide, its
CC   agonist, antagonist, or antibody that specifically binds to the
CC   polypeptide is useful for treating an immune related disorder such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease of the central or peripheral nervous
CC   system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC   a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The present sequence represents a PRO protein
CC   of the invention.
XX
SQ   Sequence 303 AA;

  Query Match             99.8%;  Score 1588;  DB 8;  Length 303;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-121;
  Matches  302;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPKAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 4
AAB07444
ID   AAB07444 standard; protein; 230 AA.
XX
AC   AAB07444;
XX
DT   20-OCT-2000  (first entry)
XX
DE   A human monocyte-derived protein FDF03DeltaTM.
XX
KW   Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
KW   FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
KW   tissue rejection; inflammation; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .17
FT                   /note= "signal peptide"
FT   Protein         18. .230
FT                   /note= "mature protein"
XX
PN   WO200040721-A1.
XX
PD   13-JUL-2000.
XX
PF   29-DEC-1999;   99WO-US030004.
XX
PR   31-DEC-1998;   98US-00223919.
PR   31-DEC-1998;   98US-00224604.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bates E,  Fournier N,  Chaulus L,  Garrone P;
XX
DR   WPI; 2000-465984/40.
DR   N-PSDB; AAA58815.
XX
PT   Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT   diseases associated with changes in monocyte numbers, e.g. bacterial or
PT   viral infections.
XX
PS   Claim 1; Page 34-35; 45pp; English.
XX
CC   The present sequence represents a human monocyte-derived protein. The
CC   specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
CC   FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
CC   regulation, or development, of haematopoietic cells. Antibodies specific
CC   for antigenic components of the proteins can be used to detect the
CC   components in samples. The proteins can also be used to screen for
CC   candidate therapeutic agents. The monocyte-derived proteins and
CC   polynucleotides can be used for diagnosis of diseases related to an
CC   increase, or decrease, in the number of monocytes in a tissue or lymph
CC   system, such as monocyte hyperplasia, tissue or graft rejection,
CC   inflammation, or bacterial or viral infections. The proteins can also be
CC   used in the treatment of disorders associated with abnormal expression or
CC   signalling by a monocyte
XX
SQ   Sequence 230 AA;

  Query Match             73.9%;  Score 1176.5;  DB 3;  Length 230;
  Best Local Similarity   75.9%;  Pred. No. 4.2e-88;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   73;  Gaps    1;
```

```
Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 227

Qy        301 LKA 303
              |||
Db        228 LKA 230
```

RESULT 5
ADE95578
ID ADE95578 standard; protein; 230 AA.
XX
AC ADE95578;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human NOVX18a protein.
XX
KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX18a.
XX
OS Homo sapiens.
XX
PN WO2003050245-A2.
XX
PD 19-JUN-2003.
XX
PF 03-DEC-2002; 2002WO-US038594.
XX
PR 05-DEC-2001; 2001US-0336600P.
PR 07-DEC-2001; 2001US-0338285P.
PR 12-DEC-2001; 2001US-0341346P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 20-DEC-2001; 2001US-0342592P.
PR 27-DEC-2001; 2001US-0344297P.
PR 31-DEC-2001; 2001US-0344903P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0406353P.
PR 31-OCT-2002; 2002US-00401788.
PR 02-DEC-2002; 2002US-00406353.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphey R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX
DR WPI; 2003-513974/48.
DR N-PSDB; ADE95577.
XX
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 110; 211pp; English.
XX
CC This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiant,
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the amino acid
CC sequence of the human NOVX18a protein of the invention.
XX
SQ Sequence 230 AA;

Query Match 73.6%; Score 1171.5; DB 7; Length 230;
Best Local Similarity 75.6%; Pred. No. 1.1e-87;
Matches 229; Conservative 0; Mismatches 1; Indels 73; Gaps 1;

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Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        168 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNENLYSV 227

Qy        301 LKA 303
              |||
Db        228 LKA 230
```

```
RESULT 6
ADE95580
ID   ADE95580 standard; protein; 206 AA.
XX
AC   ADE95580;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human NOVX18b protein.
XX
KW   NOVX protein; biochemical stimulation; physiological stimulation;
KW   cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW   antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW   immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW   nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW   antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW   NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW   cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW   psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW   Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW   depression; allergy; fertility disorder; NOVX18b.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 99
FT                   /label= OTHER
FT                   /note= "OTHER= May be substituted by Cys as a result of a
FT                   single nucleotide polymorphism"
FT   Misc-difference 147
FT                   /label= OTHER
FT                   /note= "OTHER= May be substituted by Gly as a result of a
FT                   single nucleotide polymorphism"
FT   Misc-difference 170
FT                   /label= OTHER
FT                   /note= "OTHER= May be substituted by Thr as a result of a
FT                   single nucleotide polymorphism"
XX
PN   WO2003050245-A2.
XX
PD   19-JUN-2003.
XX
PF   03-DEC-2002; 2002WO-US038594.
XX
PR   05-DEC-2001; 2001US-0336600P.
PR   07-DEC-2001; 2001US-0338285P.
PR   12-DEC-2001; 2001US-0341346P.
PR   17-DEC-2001; 2001US-0341477P.
PR   17-DEC-2001; 2001US-0341540P.
PR   20-DEC-2001; 2001US-0342592P.
PR   27-DEC-2001; 2001US-0344297P.
PR   31-DEC-2001; 2001US-0344903P.
PR   17-APR-2002; 2002US-0373288P.
PR   15-MAY-2002; 2002US-0380981P.
PR   17-MAY-2002; 2002US-0381495P.
PR   28-MAY-2002; 2002US-0383534P.
PR   28-MAY-2002; 2002US-0383744P.
PR   29-MAY-2002; 2002US-0383829P.
PR   29-MAY-2002; 2002US-0384024P.
PR   07-AUG-2002; 2002US-0401788P.
PR   26-AUG-2002; 2002US-0406353P.
PR   31-OCT-2002; 2002US-00401788.
PR   02-DEC-2002; 2002US-00406353.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Anderson DW,  Boldog FL,  Burgess CE,  Chillakuru RA;
PI   Edinger SR,  Gerlach VL,  Gorman L,  Gould-Rothberg BE,  Guo X;
PI   Jeffers ME,  Ji W,  Li L,  Malyankar UM,  Miller CE,  Murphey R;
PI   Patturajan M,  Peyman JA,  Rastelli L,  Rieger DK,  Shenoy SG;
PI   Smithson G,  Starling G,  Taupier RJ,  Voss EZ,  Zhong H,  Zhong M;
XX
DR   WPI; 2003-513974/48.
DR   N-PSDB; ADE95579.
XX
PT   New NOVX polypeptides and nucleic acids, useful for preventing or
PT   treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT   atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 2; SEQ ID NO 112; 211pp; English.
XX
CC   This invention relates to novel NOVX proteins, and the DNA sequence which
CC   encode them, having properties related to stimulation of biochemical or
CC   physiological responses in a cell, a tissue, an organ or an organism.
CC   Compounds which modulate the proteins of the invention may have cardiant,
CC   antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC   antiarthritic, antidiabetic, nephrotropic, dermatological,
CC   immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC   nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC   antidepressant, antiallergic or gynaecological activities. The DNA
CC   sequences of the invention may be useful for gene therapy whilst the
CC   protein sequences may allow the development of a vaccine. The protein is
CC   useful in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease. The invention may be useful in
CC   diagnosing, treating or preventing NOVX-associated disorders, for example
CC   cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC   rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC   disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC   Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC   fertility disorders. The nucleic acids may further be used as
CC   hybridisation probes, in chromosome mapping, tissue typing, preventive
CC   medicine, and pharmacogenomics. The present sequence is the amino acid
CC   sequence of the human NOVX18b protein of the invention.
XX
SQ   Sequence 206 AA;

  Query Match             63.5%;  Score 1010.5;  DB 7;  Length 206;
  Best Local Similarity   67.7%;  Pred. No. 1.5e-74;
  Matches  205;  Conservative    0;  Mismatches    1;  Indels   97;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              |||                         ||||||||||||||||||||||||||||||||
Db         61 LAT-----------------------SIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 96

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||
Db         97 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 127

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                  ||||||||||||||||
Db        128 ---------------------------------------------GQQRTKATTPAREPFQ 143

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        144 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNENLYSV 203

Qy        301 LKA 303
              |||
Db        204 LKA 206


RESULT 7
AAY08015
ID   AAY08015 standard; protein; 226 AA.
XX
AC   AAY08015;
XX
DT   08-JUL-1999  (first entry)
XX
DE   Human LSP-1 protein.
```

```
XX
KW   LSP-1; signal peptide; leucocyte-specific protein-1; PA-I; TAP-1; cancer;
KW   proliferin analogue I; thrombopoietin analogue protein 1; anticancer;
KW   antiangiogenic; anticancer; anti-inflammatory; anti-thrombocytopenic;
KW   anti-arthritic; signal transduction; inflammatory; disease; growth;
KW   proliferation; differentiation; cell survival; angiogenesis; diagnosis;
KW   haematopoietic stem cell; erythroid precursor; megakaryocytopoiesis;
KW   thrombopoiesis; prognosis; treatment; chromosome mapping; tissue typing;
KW   forensic; arthritis; thrombocytopenia; bone marrow transplant; infection;
KW   intravascular coagulation: iron deficiency; HIV; human.
XX
OS   Homo sapiens.
XX
PN   WO9918243-A1.
XX
PD   15-APR-1999.
XX
PF   06-OCT-1998;   98WO-US021151.
XX
PR   06-OCT-1997;   97US-0061143P.
PR   06-OCT-1997;   97US-0061149P.
PR   06-OCT-1997;   97US-0061159P.
PR   08-JAN-1998;   98US-00004206.
PR   22-JAN-1998;   98US-00010674.
PR   27-JAN-1998;   98US-00014347.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Pan Y,  Gearing DP,  Mccarthy SA;
XX
DR   WPI; 1999-264042/22.
DR   N-PSDB; AAX37558.
XX
PT   Signal-peptide containing proteins that modulate cellular processes.
XX
PS   Claim 2; Fig 1; 124pp; English.
XX
CC   This invention describes the isolation of nucleic acids encoding the
CC   signal-peptide-containing molecules leucocyte-specific protein-1 (LSP-1),
CC   proliferin analog I (PA-I) and thrombopoietin analog protein 1 (TAP-1).
CC   These proteins have antiangiogenic, anticancer, anti-inflammatory, anti-
CC   arthritic and anti-thrombocytopenic activity. The products of the
CC   invention and their modulators are involved in signal transduction,
CC   inflammatory responses, growth, proliferation, differentiation and
CC   survival of cells; angiogenesis; maturation of haematopoietic stem cells
CC   and erythroid precursors megakaryocytopoiesis and thrombopoiesis.
CC   Antibodies, or other binding agents, specific for the products of the
CC   invention are useful for diagnosis, prognosis and monitoring of treatment
CC   of diseases. Other uses include chromosome mapping, identification of
CC   individuals (tissue typing) and in forensic studies. LSP-1, PA-I and TAP-
CC   1 proteins and nucleic acids are modulators of cellular processes,
CC   particularly they are used to treat or prevent diseases associated with
CC   deregulation of angiogenesis, immune responses and haematopoiesis, e.g.
CC   cancer, arthritis (and other inflammatory diseases), thrombocytopenia
CC   (caused by cancer treatment, bone marrow transplant, human immune
CC   deficiency virus infection etc.), intravascular coagulation, iron
CC   deficiency etc
XX
SQ   Sequence 226 AA;

  Query Match             61.2%;  Score 973.5;  DB 2;  Length 226;
  Best Local Similarity   82.5%;  Pred. No. 1.8e-71;
  Matches  188;  Conservative   14;  Mismatches   17;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 8
AAB07447
ID   AAB07447 standard; protein; 226 AA.
XX
AC   AAB07447;
XX
DT   20-OCT-2000  (first entry)
XX
DE   A human monocyte-derived protein FDF03-S2.
XX
KW   Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
KW   FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
KW   tissue rejection; inflammation; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .17
FT                   /note= "signal sequence"
FT   Protein         18. .226
FT                   /note= "mature protein"
XX
PN   WO200040721-A1.
XX
PD   13-JUL-2000.
XX
PF   29-DEC-1999;   99WO-US030004.
XX
PR   31-DEC-1998;   98US-00223919.
PR   31-DEC-1998;   98US-00224604.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bates E,  Fournier N,  Chaulus L,  Garrone P;
XX
DR   WPI; 2000-465984/40.
DR   N-PSDB; AAA58818.
XX
PT   Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT   diseases associated with changes in monocyte numbers, e.g. bacterial or
PT   viral infections.
XX
PS   Claim 1; Page 41-42; 45pp; English.
XX
CC   The present sequence represents a human monocyte-derived protein. The
CC   specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
CC   FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
CC   regulation, or development, of haematopoietic cells. Antibodies specific
CC   for antigenic components of the proteins can be used to detect the
CC   components in samples. The proteins can also be used to screen for
CC   candidate therapeutic agents. The monocyte-derived proteins and
CC   polynucleotides can be used for diagnosis of diseases related to an
CC   increase, or decrease, in the number of monocytes in a tissue or lymph
CC   system, such as monocyte hyperplasia, tissue or graft rejection,
CC   inflammation, or bacterial or viral infections. The proteins can also be
CC   used in the treatment of disorders associated with abnormal expression or
CC   signalling by a monocyte
XX
SQ   Sequence 226 AA;

  Query Match             61.2%;  Score 973.5;  DB 3;  Length 226;
  Best Local Similarity   82.5%;  Pred. No. 1.8e-71;
  Matches  188;  Conservative   14;  Mismatches   17;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
```

```
                ||||||||||  || |||||||  ||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
               ||||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
               |||||||||||| ||||| |||:||||:|||||||          |||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
               |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 9
AAW80407
ID   AAW80407 standard; protein; 226 AA.
XX
AC   AAW80407;
XX
DT   25-MAR-2003  (revised)
DT   13-JAN-1999  (first entry)
XX
DE   A secreted protein encoded by clone di39_9.
XX
KW   Secreted protein; immune stimulating; suppressing;
KW   haematopoiesis regulating activity; tissue growth activity; activin;
KW   inhibin activity; chemotactic; chemokinetic activity; haemostatic;
KW   thrombolytic activity; anti-inflammatory activity; cadherin;
KW   tumour invasion suppressor activity; tumour inhibition activity.
XX
OS   Homo sapiens.
XX
PN   WO9844113-A1.
XX
PD   08-OCT-1998.
XX
PF   27-MAR-1998;   98WO-US006176.
XX
PR   28-MAR-1997;   97US-00823330.
PR   25-MAR-1998;   98US-00047661.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Spaulding V,  Agostino MJ;
XX
DR   WPI; 1998-542703/46.
DR   N-PSDB; AAV63191.
XX
PT   New isolated polynucleotide(s) and secreted proteins - are obtained from
PT   human cDNA libraries prepared from adult testes, foetal brain, adult
PT   brain, adult blood and placenta.
XX
PS   Claim 19; Page 76-77; 124pp; English.
XX
CC   The present sequence represents a secreted protein. The nucleic acid
CC   sequence is isolated from a human adult testes cDNA library using probe
CC   AAV63202. The polypeptide may have biological activities such has e.g.
CC   nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity or other activities. (Updated on 25-MAR-2003 to correct PR
CC   field.)
XX
SQ   Sequence 226 AA;

  Query Match           60.8%;  Score 967.5;  DB 2;  Length 226;
  Best Local Similarity 82.0%;  Pred. No. 5.5e-71;
  Matches  187;  Conservative   14;  Mismatches   18;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
               ||||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
               |||||||||||| ||||| |||:||||:|||||||          |||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWTPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
               |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 10
ABP61825
ID   ABP61825 standard; protein; 226 AA.
XX
AC   ABP61825;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Human polypeptide SEQ ID NO 179.
XX
KW   Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic;
KW   antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
KW   neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
KW   antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW   immunostimulant; antiparasitic; secreted protein; transmembrane protein;
KW   cytokine; cell proliferation; cell differentiation; autoimmune disease;
KW   stem cell; growth factor; nervous system disease; neuropathy;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW   osteoporosis; severe combined immunodeficiency; SCID; infection;
KW   multiple sclerosis; rheumatoid arthritis; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002065394-A1.
XX
PD   30-MAY-2002.
XX
PF   22-DEC-2000; 2000US-00745763.
XX
PR   18-MAR-1998;   98US-00040963.
XX
PA   (JACO/) JACOBS K.
PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (SPAU/) SPAULDING V.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Spaulding V;
XX
DR   WPI; 2002-582343/62.
DR   N-PSDB; ABQ92041.
XX
PT   Novel secreted or transmembrane protein and polynucleotide encoding the
PT   protein, useful for diagnosis and treatment of neurological disorders,
PT   cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
XX
PS   Claim 136; Page 159; 284pp; English.
XX
CC   The invention relates to human secreted or transmembrane protein (I),
CC   their fragments and is encoded by specific complementary deoxyribonucleic
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CC   acid (cDNA) inserts (II), where the protein is substantially free from
CC   other mammalian proteins. (I) are useful for preventing, treating or
CC   ameliorating a medical condition, especially immunological treatment or
CC   prevention of tumours. (I) exhibits activity relating to angiogenesis,
CC   cytokine, cell proliferation, cell differentiation, antiinflammatory,
CC   stem cell growth factor activity and activin or inhibin-related
CC   activities. (I) can be used to manipulate stem cells in culture to give
CC   rise to neuroepithelial cells that can be used to augment or replace
CC   cells damaged by illness, autoimmune disease, accidental damage or
CC   genetic disorders. (I) induces the proliferation of neural cells and
CC   regeneration of nerve and brain tissue and is useful for the treatment of
CC   central and peripheral nervous system diseases and neuropathies, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis. (I) is involved in chemotactic or chemokinetic
CC   activity, regulation of haematopoiesis and is useful for treating myeloid
CC   or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
CC   and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC   tissue growth and in tissue repair, healing of burns, incisions, ulcers,
CC   for treating osteoporosis, osteoarthritis, bone degenerative disorders or
CC   periodontal disease. (I) is also useful for gut protection or
CC   regeneration and treatment of lung or liver fibrosis, reperfusion injury
CC   in various tissues, various immune deficiencies and disorders including
CC   severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC   autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
CC   diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
CC   such as asthma or other respiratory problems. (II) is useful to express
CC   recombinant protein, as markers for tissues in which the corresponding
CC   protein is preferentially expressed and in gene therapy. The present
CC   sequence is that of a polypeptide of the invention
XX
SQ   Sequence 226 AA;

  Query Match             60.8%;  Score 967.5;  DB 5;  Length 226;
  Best Local Similarity   82.0%;  Pred. No. 5.5e-71;
  Matches  187;  Conservative   14;  Mismatches   18;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||       ||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWTPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 11
AAB07445
ID   AAB07445 standard; protein; 227 AA.
XX
AC   AAB07445;
XX
DT   20-OCT-2000  (first entry)
XX
DE   A human monocyte-derived protein FDF03-S1.
XX
KW   Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
KW   FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
KW   tissue rejection; inflammation; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .17
FT                   /note= "signal sequence"
FT   Protein         18. .227
FT                   /note= "mature protein"
XX
PN   WO200040721-A1.
XX
PD   13-JUL-2000.
XX
PF   29-DEC-1999;   99WO-US030004.
XX
PR   31-DEC-1998;   98US-00223919.
PR   31-DEC-1998;   98US-00224604.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bates E,  Fournier N,  Chaulus L,  Garrone P;
XX
DR   WPI; 2000-465984/40.
DR   N-PSDB; AAA58816.
XX
PT   Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT   diseases associated with changes in monocyte numbers, e.g. bacterial or
PT   viral infections.
XX
PS   Claim 1; Page 37-38; 45pp; English.
XX
CC   The present sequence represents a human monocyte-derived protein. The
CC   specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
CC   FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
CC   regulation, or development, of haematopoietic cells. Antibodies specific
CC   for antigenic components of the proteins can be used to detect the
CC   components in samples. The proteins can also be used to screen for
CC   candidate therapeutic agents. The monocyte-derived proteins and
CC   polynucleotides can be used for diagnosis of diseases related to an
CC   increase, or decrease, in the number of monocytes in a tissue or lymph
CC   system, such as monocyte hyperplasia, tissue or graft rejection,
CC   inflammation, or bacterial or viral infections. The proteins can also be
CC   used in the treatment of disorders associated with abnormal expression or
CC   signalling by a monocyte
XX
SQ   Sequence 227 AA;

  Query Match             60.2%;  Score 958;  DB 3;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 3.3e-70;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:|||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||         ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 221


RESULT 12
ABU89824
ID   ABU89824 standard; protein; 227 AA.
XX
AC   ABU89824;
XX
DT   10-JUL-2003  (first entry)
XX
DE   TNF-receptor associated factor 5 (TRAF5) interacting protein #4.
XX
KW   Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;
KW   TNF-receptor associated factor 5 interacting protein;
```

```
KW   tumour necrosis factor associated factor 5 interacting protein;
KW   TRAF5 interacting protein.
XX
OS   Homo sapiens.
XX
PN   WO2003031571-A2.
XX
PD   17-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031357.
XX
PR   05-OCT-2001; 2001US-0327454P.
PR   09-OCT-2001; 2001US-0327917P.
PR   09-OCT-2001; 2001US-0328029P.
PR   09-OCT-2001; 2001US-0328056P.
PR   12-OCT-2001; 2001US-0328849P.
PR   15-OCT-2001; 2001US-0329414P.
PR   17-OCT-2001; 2001US-0330142P.
PR   22-OCT-2001; 2001US-0341058P.
PR   24-OCT-2001; 2001US-0343629P.
PR   29-OCT-2001; 2001US-0349575P.
PR   01-NOV-2001; 2001US-0346357P.
PR   25-JUN-2002; 2002US-0391342P.
PR   01-OCT-2002; 2002US-00262445.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Burgess CE,  Catterton E,  Chant JS,  Chaudhuri A;
PI   Edinger SR,  Gerlach VL,  Giot L,  Gorman L,  Guo X,  Kekuda R;
PI   Mezes PS,  Millet I,  Ooi CE,  Patturajan M,  Rieger DK,  Spytek KA;
PI   Taupier RJ,  Zerhusen BD,  Zhong H,  Zhong M;
XX
DR   WPI; 2003-381704/36.
DR   N-PSDB; ACA90240.
XX
PT   New DAPK3 polypeptide, useful for preparing a composition for treating or
PT   preventing e.g., cancer.
XX
PS   Example 20F; Page 242; 253pp; English.
XX
CC   The invention describes an isolated polypeptide comprising any of 33 90-
CC   1273 amino acid sequences (I) given in the specification or its mature
CC   form, a sequence that is at least 95 % identical to (I), or a sequence
CC   comprising one or more conservative substitutions in the amino acid
CC   sequence of (I). The polypeptide is useful for preparing a composition
CC   for treating or preventing e.g. cancer. This is the amino acid sequence
CC   of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
CC   interacting protein associated with the identification of novel human
CC   proteins and their functions
XX
SQ   Sequence 227 AA;

  Query Match             60.2%;  Score 958;  DB 6;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 3.3e-70;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:|||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        |||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221
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```
RESULT 13
AAW63682
ID   AAW63682 standard; protein; 291 AA.
XX
AC   AAW63682;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Human secreted protein 2.
XX
KW   Secreted protein; human; cell proliferation; cytokine activity;
KW   tissue growth; cellular differentiation; regeneration; activin; inhibin;
KW   chemotactic; haemostatic; thrombolytic; tumour inhibition;
KW   anti-inflammatory activity; biomarker.
XX
OS   Homo sapiens.
XX
PN   WO9825959-A2.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US022787.
XX
PR   11-DEC-1996;   96US-0032757P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Escobedo J,  Hu Q,  Garcia P,  Williams LT,  Kothakota S;
XX
DR   WPI; 1998-348453/30.
DR   N-PSDB; AAV43602.
XX
PT   Secreted human polypeptides - having cytokine, cell proliferation or
PT   differentiation, activin or inhibin, tumour inhibition or anti-
PT   inflammatory activities.
XX
PS   Claim 1; Page 49-50; 78pp; English.
XX
CC   This represents a human secreted protein. The specification provides
CC   secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic
CC   acid sequences shown in AAV43601 to AAV43619. The invention provides a
CC   method of identifying a secreted polypeptide which is modified by rough
CC   microsomes. The secreted proteins can be used in assays to determine
CC   biological activities, such as cytokine, cell proliferation, or cellular
CC   differentiation activities, tissue growth or regeneration, activin or
CC   inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC   thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC   anti-inflammatory activity. The proteins can also be used as biomarkers,
CC   to identify tissues or cell types which express the proteins, or a stage-
CC   or disease-specific alteration in protein expression. They can be used in
CC   protein interaction assays, to identify ligands or binding proteins.
CC   Compounds which affect the biological activities of the secreted proteins
CC   or their ability to interact with specific ligands can be identified
CC   using the proteins in screening assays. The proteins and antibodies that
CC   bind specifically to the protein can also be used to design diagnostic
CC   tests and therapeutic compositions for diseases which may be associated
CC   with altered expression of these proteins. Fusion proteins comprising,
CC   e.g. signal sequences or transmembrane domains of the proteins can be
CC   used to target other protein domains to cellular membrane or they can be
CC   secreted extracellularly
XX
SQ   Sequence 291 AA;

  Query Match             60.2%;  Score 958;  DB 2;  Length 291;
  Best Local Similarity   80.8%;  Pred. No. 4.5e-70;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| |||||||||||||||||||||||||||||||||||||
Db         65 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 124

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:|||||||||||||||||||||||||||||||||||:|||||||||:|:||
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Db        125 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 184

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        185 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 236

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        237 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 285


RESULT 14
ABB12010
ID   ABB12010 standard; peptide; 326 AA.
XX
AC   ABB12010;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human secreted protein homologue, SEQ ID NO:2380.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US003800.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   N-PSDB; ABA09254.
XX
PT   Human proteins and DNA encoding sequences useful for preventing, treating
PT   or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT   and cancer.
XX
PS   Claim 20; Page 295; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a novel human
CC   polypeptide of the invention
XX
SQ   Sequence 326 AA;

  Query Match             60.2%;  Score 958;  DB 4;  Length 326;
  Best Local Similarity   80.8%;  Pred. No. 5.3e-70;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| |||||||||||||||||||||||||||||||||||||
Db        100 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 159

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:|||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db        160 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 219

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        220 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 271

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        272 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 320


RESULT 15
AAY87230
ID   AAY87230 standard; protein; 227 AA.
XX
AC   AAY87230;
XX
DT   11-MAY-2000  (first entry)
XX
DE   Human signal peptide containing protein HSPP-7 SEQ ID NO:7.
XX
KW   Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW   inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW   antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW   antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW   reproductive disorder; developmental disorder; arteriosclerosis;
KW   cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW   asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW   Parkinson's disease; Huntington's diseases; ovulatory defect;
KW   muscular dystrophy.
XX
OS   Homo sapiens.
XX
PN   WO200000610-A2.
XX
PD   06-JAN-2000.
XX
```

PF 25-JUN-1999; 99WO-US014484.
XX
PR 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.
PR 11-DEC-1998; 98US-0112129P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR N-PSDB; AAZ98115.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.
XX
PS Claim 1; Page 164-165; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSPP, for
CC detecting HSPP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSPP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSPP from natural
CC sources
XX
SQ Sequence 227 AA;

Query Match 59.4%; Score 945; DB 3; Length 227;
Best Local Similarity 79.9%; Pred. No. 3.8e-69;
Matches 183; Conservative 15; Mismatches 21; Indels 10; Gaps 2;

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Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||  ||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSXXYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||   |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221
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Search completed: June 1, 2005, 22:08:23
Job time : 165 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 1, 2005, 22:05:46 ; Search time 142 Seconds
(without alignments)
737.613 Million cell updates/sec

Title: US-10-777-524-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLPLLLPPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1591	100.0	303	10	US-09-774-381-58	Sequence 58, Appl
2	1591	100.0	303	14	US-10-290-631-2	Sequence 2, Appli
3	1591	100.0	303	16	US-10-780-043-2	Sequence 2, Appli
4	1591	100.0	303	16	US-10-777-524-2	Sequence 2, Appli
5	1591	100.0	303	17	US-10-777-521-2	Sequence 2, Appli
6	1176.5	73.9	230	16	US-10-780-043-4	Sequence 4, Appli
7	1171.5	73.6	230	15	US-10-309-290-110	Sequence 110, App
8	1010.5	63.5	206	15	US-10-309-290-112	Sequence 112, App
9	973.5	61.2	226	10	US-09-774-381-44	Sequence 44, Appl
10	973.5	61.2	226	16	US-10-780-043-10	Sequence 10, Appl
11	967.5	60.8	226	9	US-09-745-763-106	Sequence 106, App
12	958	60.2	227	15	US-10-262-445-128	Sequence 128, App
13	958	60.2	227	16	US-10-780-043-6	Sequence 6, Appli
14	958	60.2	291	9	US-09-935-390A-21	Sequence 21, Appl
15	958	60.2	326	15	US-10-276-774-2380	Sequence 2380, Ap
16	934	58.7	238	10	US-09-809-391-485	Sequence 485, App
17	934	58.7	238	10	US-09-882-171-485	Sequence 485, App
18	934	58.7	238	15	US-10-164-861-485	Sequence 485, App
19	821	51.6	175	16	US-10-780-043-8	Sequence 8, Appli
20	517	32.5	101	10	US-09-809-391-754	Sequence 754, App
21	517	32.5	101	10	US-09-882-171-754	Sequence 754, App
22	517	32.5	101	15	US-10-164-861-754	Sequence 754, App
23	411	25.8	224	10	US-09-866-050A-711	Sequence 711, App
24	222	14.0	99	14	US-10-290-631-4	Sequence 4, Appli
25	222	14.0	99	16	US-10-777-524-4	Sequence 4, Appli
26	222	14.0	99	17	US-10-777-521-4	Sequence 4, Appli
27	148.5	9.3	305	15	US-10-291-265-391	Sequence 391, App
28	146.5	9.2	305	10	US-09-796-753-104	Sequence 104, App
29	146.5	9.2	305	10	US-09-796-753-120	Sequence 120, App
30	146.5	9.2	305	15	US-10-291-265-863	Sequence 863, App
31	139	8.7	290	9	US-09-965-529-18	Sequence 18, Appl
32	139	8.7	290	10	US-09-969-680A-18	Sequence 18, Appl
33	139	8.7	290	14	US-10-227-884-40	Sequence 40, Appl
34	139	8.7	290	14	US-10-230-163-40	Sequence 40, Appl
35	139	8.7	290	14	US-10-230-338-40	Sequence 40, Appl
36	139	8.7	290	14	US-10-218-631-40	Sequence 40, Appl
37	139	8.7	290	14	US-10-230-414-40	Sequence 40, Appl
38	139	8.7	290	14	US-10-232-224-40	Sequence 40, Appl
39	139	8.7	290	14	US-10-216-159A-40	Sequence 40, Appl
40	139	8.7	290	14	US-10-218-849-40	Sequence 40, Appl
41	139	8.7	290	14	US-10-227-873-40	Sequence 40, Appl
42	139	8.7	290	14	US-10-227-883-40	Sequence 40, Appl
43	139	8.7	290	14	US-10-219-076-40	Sequence 40, Appl
44	139	8.7	290	14	US-10-230-434-40	Sequence 40, Appl
45	139	8.7	290	14	US-10-219-003-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-774-381-58
; Sequence 58, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19

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;  NUMBER OF SEQ ID NOS:  59
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 58
;   LENGTH: 303
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-774-381-58

  Query Match             100.0%;  Score 1591;  DB 10;  Length 303;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-126;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
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Db        301 LKA 303


RESULT 2
US-10-290-631-2
; Sequence 2, Application US/10290631
; Publication No. US20030105303A1
;   GENERAL INFORMATION:
;        APPLICANT: Adema, Gosse Jan
;                   Meyaard, Linde
;                   Gorman, Daniel M.
;                   McClanahan, Terrill K.
;                   Zurawski, Sandra M.
;                   Zurawski, Gerard
;                   Lanier, Lewis L.
;                   Phillips Jr., Joseph H.
;        TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                            Related Reagents
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/290,631
;             FILING DATE: 08-No. US20030105303A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/985,950
;             FILING DATE: 05-DEC-1997
;             APPLICATION NUMBER: US 60/041,279
;             FILING DATE: 21-MARCH-1997
;             APPLICATION NUMBER: US 60/033,181
;             FILING DATE: 16-DEC-1996
;             APPLICATION NUMBER: US 60/032,252
;             FILING DATE: 06-DEC-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0670K
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650)852-9196
;             TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 303 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-631-2

  Query Match             100.0%;  Score 1591;  DB 14;  Length 303;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-126;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
              |||
Db        301 LKA 303


RESULT 3
US-10-780-043-2
; Sequence 2, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/10/780,043
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER: US/09/869,388
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 2
;   LENGTH: 303
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-780-043-2
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  Query Match           100.0%;  Score 1591;  DB 16;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-126;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
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Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
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Db        301 LKA 303


RESULT 4
US-10-777-524-2
; Sequence 2, Application US/10777524
; Publication No. US20040143858A1
;   GENERAL INFORMATION:
;        APPLICANT: Adema, Gosse Jan
;                   Meyaard, Linde
;                   Gorman, Daniel M.
;                   McClanahan, Terrill K.
;                   Zurawski, Sandra M.
;                   Zurawski, Gerard
;                   Lanier, Lewis L.
;                   Phillips Jr., Joseph H.
;        TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                            Related Reagents
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/777,524
;             FILING DATE: 11-Feb-2004
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/546,049
;             FILING DATE: 10-Apr-2000
;             APPLICATION NUMBER: US/08/985,950
;             FILING DATE: 05-DEC-1997
;             APPLICATION NUMBER: US 60/041,279
;             FILING DATE: 21-MARCH-1997
;             APPLICATION NUMBER: US 60/033,181
;             FILING DATE: 16-DEC-1996
;             APPLICATION NUMBER: US 60/032,252
;             FILING DATE: 06-DEC-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0670K
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650)852-9196
;             TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 303 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-777-524-2

  Query Match           100.0%;  Score 1591;  DB 16;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-126;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
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Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
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Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
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Db        301 LKA 303


RESULT 5
US-10-777-521-2
; Sequence 2, Application US/10777521
; Publication No. US20050059808A1
;   GENERAL INFORMATION:
;        APPLICANT: Adema, Gosse Jan
;                   Meyaard, Linde
;                   Gorman, Daniel M.
;                   McClanahan, Terrill K.
;                   Zurawski, Sandra M.
;                   Zurawski, Gerard
;                   Lanier, Lewis L.
;                   Phillips Jr., Joseph H.
;        TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                            Related Reagents
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/777,521
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;            FILING DATE: 11-Feb-2004
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/546,049
;            FILING DATE: 10-Apr-2000
;            APPLICATION NUMBER: US/08/985,950
;            FILING DATE: 05-DEC-1997
;            APPLICATION NUMBER: US 60/041,279
;            FILING DATE: 21-MARCH-1997
;            APPLICATION NUMBER: US 60/033,181
;            FILING DATE: 16-DEC-1996
;            APPLICATION NUMBER: US 60/032,252
;            FILING DATE: 06-DEC-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ching, Edwin P.
;            REGISTRATION NUMBER: 34,090
;            REFERENCE/DOCKET NUMBER: DX0670K
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650)852-9196
;            TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 303 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-777-521-2

  Query Match            100.0%;  Score 1591;  DB 17;  Length 303;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-126;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
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Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
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Db        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300

Qy        301 LKA 303
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Db        301 LKA 303


RESULT 6
US-10-780-043-4
; Sequence 4, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/10/780,043
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER: US/09/869,388
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 4
;   LENGTH: 230
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-780-043-4

  Query Match            73.9%;  Score 1176.5;  DB 16;  Length 230;
  Best Local Similarity  75.9%;  Pred. No. 3.7e-91;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   73;  Gaps    1;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151
              ||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
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Db        168 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 227

Qy        301 LKA 303
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Db        228 LKA 230


RESULT 7
US-10-309-290-110
; Sequence 110, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Chillakuru, Rajeev A.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Gould-Rothberg, Bonnie E.
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Jeffers, Michael E.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Li, Li
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Murphey, Ryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Starling, Gary
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-502A
;  CURRENT APPLICATION NUMBER: US/10/309,290
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/336,600
```

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;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: 60/338,285
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 60/341,346
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: 60/341,477
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/341,540
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/342,592
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/344,297
;  PRIOR FILING DATE: 2001-12-27
;  PRIOR APPLICATION NUMBER: 60/344,903
;  PRIOR FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/373,288
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/380,981
;  PRIOR FILING DATE: 2002-05-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 110
;   LENGTH: 230
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-290-110

  Query Match             73.6%;  Score 1171.5;  DB 15;  Length 230;
  Best Local Similarity   75.6%;  Pred. No. 9.7e-91;
  Matches  229;  Conservative    0;  Mismatches    1;  Indels   73;  Gaps    1;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||
Db        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 151

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
Db        152 ----------------------------------------GQQRTKATTPAREPFQ 167

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNENLYSV 227

Qy        301 LKA 303
              |||
Db        228 LKA 230


RESULT 8
US-10-309-290-112
; Sequence 112, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Chillakuru, Rajeev A.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Gould-Rothberg, Bonnie E.
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Jeffers, Michael E.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Li, Li
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Murphey, Ryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Starling, Gary
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-502A
;  CURRENT APPLICATION NUMBER: US/10/309,290
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/336,600
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: 60/338,285
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 60/341,346
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: 60/341,477
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/341,540
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/342,592
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/344,297
;  PRIOR FILING DATE: 2001-12-27
;  PRIOR APPLICATION NUMBER: 60/344,903
;  PRIOR FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/373,288
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/380,981
;  PRIOR FILING DATE: 2002-05-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 112
;   LENGTH: 206
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-290-112

  Query Match             63.5%;  Score 1010.5;  DB 15;  Length 206;
  Best Local Similarity   67.7%;  Pred. No. 3.3e-77;
  Matches  205;  Conservative    0;  Mismatches    1;  Indels   97;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              |||                          ||||||||||||||||||||||||||||||
Db         61 LAT-----------------------SIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 96

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              ||||||||||||||||||||||||||||||
Db         97 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ---------------------------- 127

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
                                                      ||||||||||||||||
Db        128 ----------------------------------------GQQRTKATTPAREPFQ 143

Qy        241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNENLYSV 203
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Qy        301 LKA 303
              |||
Db        204 LKA 206


RESULT 9
US-09-774-381-44
; Sequence 44, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
;  APPLICANT:  Holtzman, Douglas A.
;  APPLICANT:  McCarthy, Sean A.
;  APPLICANT:  Pan, Yang
;  APPLICANT:  Gearing, David P.
;  TITLE OF INVENTION:  NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE:  MNI-107CP2
;  CURRENT APPLICATION NUMBER: US/09/774,381
;  CURRENT FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER:  08/941,354
;  PRIOR FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER:  09/010,674
;  PRIOR FILING DATE:  1998-01-22
;  PRIOR APPLICATION NUMBER:  60/061,149
;  PRIOR FILING DATE:  1997-10-06
;  PRIOR APPLICATION NUMBER:  09/014,347
;  PRIOR FILING DATE:  1998-01-27
;  PRIOR APPLICATION NUMBER:  60/061,159
;  PRIOR FILING DATE:  1997-10-06
;  PRIOR APPLICATION NUMBER:  09/474,151
;  PRIOR FILING DATE:  2000-12-21
;  PRIOR APPLICATION NUMBER:  09/004,206
;  PRIOR FILING DATE:  1998-01-08
;  PRIOR APPLICATION NUMBER:  60/061,143
;  PRIOR FILING DATE:  1997-10-06
;  PRIOR APPLICATION NUMBER:  09/483,414
;  PRIOR FILING DATE:  2000-01-14
;  PRIOR APPLICATION NUMBER:  09/213,571
;  PRIOR FILING DATE:  1998-12-18
;  PRIOR APPLICATION NUMBER:  08/994,890
;  PRIOR FILING DATE:  1997-12-19
;  NUMBER OF SEQ ID NOS:  59
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-774-381-44

  Query Match             61.2%;  Score 973.5;  DB 10;  Length 226;
  Best Local Similarity   82.5%;  Pred. No. 5e-74;
  Matches  188;  Conservative   14;  Mismatches   17;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 10
US-10-780-043-10
; Sequence 10, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/10/780,043
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER: US/09/869,388
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 10
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-780-043-10

  Query Match             61.2%;  Score 973.5;  DB 16;  Length 226;
  Best Local Similarity   82.5%;  Pred. No. 5e-74;
  Matches  188;  Conservative   14;  Mismatches   17;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||        ||||| |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
              |: |  |:|||:||:||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 11
US-09-745-763-106
; Sequence 106, Application US/09745763
; Patent No. US20020065394A1
;   GENERAL INFORMATION:
;        APPLICANT: Jacobs, Kenneth
;                   McCoy, John M.
;                   LaVallie, Edward R.
;                   Collins-Racie, Lisa A.
;                   Evans, Cheryl
;                   Merberg, David
;                   Treacy, Maurice
;                   Spaulding, Vikki
;        TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
;                            ENCODING THEM
;        NUMBER OF SEQUENCES: 219
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: MA
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/745,763
;             FILING DATE: 18-Jun-2000
;             CLASSIFICATION: <Unknown>
```

```
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sprunger, Suzanne A.
;             REGISTRATION NUMBER: 41,323
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 498-8284
;             TELEFAX: (617) 876-5851
;    INFORMATION FOR SEQ ID NO: 106:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 226 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-745-763-106

  Query Match             60.8%;  Score 967.5;  DB 9;  Length 226;
  Best Local Similarity   82.0%;  Pred. No. 1.6e-73;
  Matches  187;  Conservative   14;  Mismatches   18;  Indels    9;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||:|:||
Db         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||          ||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWTPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR-WRRRKGQQ 227
              |: |  |:|||:||::||: ||:|| ||  :||||:|||  |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSR 220


RESULT 12
US-10-262-445-128
; Sequence 128, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John
;  APPLICANT:  Burgess, Catherine
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chant, John
;  APPLICANT:  Chaudhuri, Amitabha
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Giot, Loic
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Mezes, Peter
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Ooi, Chean Eng
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS O
;  TITLE OF INVENTION:  THE SAME
;  FILE REFERENCE: 21402-462D
;  CURRENT APPLICATION NUMBER: US/10/262,445
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/327,454
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: 60/327,917
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,029
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,056
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,849
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: 60/329,414
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/330,142
;  PRIOR FILING DATE: 2001-10-17
;  PRIOR APPLICATION NUMBER: 60/341,058
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 60/343,629
;  PRIOR FILING DATE: 2001-10-24
;  PRIOR APPLICATION NUMBER: 60/349,575
;  PRIOR FILING DATE: 2001-10-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 128
;   LENGTH: 227
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-262-445-128

  Query Match             60.2%;  Score 958;  DB 15;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 1e-72;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
              |||||||||| || ||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
              ||  |:||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
              |||||||||||| ||||| |||:||||:|||||||          ||||  |||||  ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
              |: |  |:|||:||::||: ||:|| ||  :||||:|||   |||||| :
Db        173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221


RESULT 13
US-10-780-043-6
; Sequence 6, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Elizabeth
;  APPLICANT:  Fournier, Nathalie
;  APPLICANT:  Chalus, Lionel
;  APPLICANT:  Garrone, Pierre
;  TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
;  FILE REFERENCE: SF0977X
;  CURRENT APPLICATION NUMBER: US/10/780,043
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER: US/09/869,388
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: IBM PC compatible
; SEQ ID NO 6
;   LENGTH: 227
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-780-043-6

  Query Match             60.2%;  Score 958;  DB 16;  Length 227;
  Best Local Similarity   80.8%;  Pred. No. 1e-72;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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                ||||||||||  || |||||||  ||||||||||||||||||||||||||||||||||||||||
Db          1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
               ||  |:||||||||||||||||||||||||||||||||||||||||:|||||||||:|:||
Db         61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
               ||||||||||||  |||||  |||:||||:|||||||         |||||  |||||   ||||
Db        121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 172

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
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RESULT 14
US-09-935-390A-21
; Sequence 21, Application US/09935390A
; Patent No. US20020076761A1
;   GENERAL INFORMATION:
;        APPLICANT: Escobedo, Jaime
;                   Quianjin, Hu
;                   Garcia, Pablo
;                   Williams, Lewis T.
;                   Kothakota, Srinivas
;        TITLE OF INVENTION: Secreted Human Proteins
;        NUMBER OF SEQUENCES: 38
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Chiron Corporation
;             STREET: 4560 Horton Street
;             CITY: Emeryville
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94608-2916
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/935,390A
;             FILING DATE: 22-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/988,671
;             FILING DATE: 1997-12-11
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane E. R. Potter
;             REGISTRATION NUMBER: 33,332
;             REFERENCE/DOCKET NUMBER: 1369.002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (510) 923-2718
;             TELEFAX: (510) 655-3542
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 291 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20020076761A1e
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-935-390A-21

  Query Match            60.2%;  Score 958;  DB 9;  Length 291;
  Best Local Similarity  80.8%;  Pred. No. 1.4e-72;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
                ||||||||||  || |||||||  ||||||||||||||||||||||||||||||||||||||||
Db         65 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 124

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
               ||||||||||||  |||||  |||:||||:|||||||         |||||  |||||   ||||
Db        185 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 236

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
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Db        237 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 285


RESULT 15
US-10-276-774-2380
; Sequence 2380, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 2380
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-276-774-2380

  Query Match            60.2%;  Score 958;  DB 15;  Length 326;
  Best Local Similarity  80.8%;  Pred. No. 1.6e-72;
  Matches  185;  Conservative   15;  Mismatches   19;  Indels   10;  Gaps    2;

Qy          1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
                ||||||||||  || |||||||  ||||||||||||||||||||||||||||||||||||||||
Db        100 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 159

Qy         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Db        160 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 219

Qy        121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTTTGLRV 180
               ||||||||||||  |||||  |||:||||:|||||||         |||||  |||||   ||||
Db        220 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTT--------TTTWRPSSTTTIAGLRV 271

Qy        181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLR--WRRRKGQQ 227
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Search completed: June  1, 2005, 22:17:18
Job time : 144 secs
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